#### STIC-Biot ch/ChemLib



From: Sent: To:

Subject:

Hamud, Fozia

Wednesday, January 22, 2003 3:59 PM STIC-Biotech/ChemLib

sequence search for 09/714,792

Please, search SEQ ID NO: 4 of 09/714, 792 against commercial and interference data bases. Thanks.

Fozia Hamud Patent Examiner Art Unit 1647 Crystal-Mall-One, Room 10Bo5 Mail Box CM1-10B19 308-8891

Point of Contact P. Sheppard Telephone number: (703) 308-4499

Searcher:
Phone:
Location:
Date Picked Up:
Date Completed: 1/29/03
Searcher Prep/Review:
Clerical:
Online time:

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

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RC TISSUE-Testis;  RA Donaldson D.D., Whitters M.J., Fitz L., Neben T., Finnerty H.,  RA Henderson S.L., O'Hara R.M. Jr., Turner K.J., Wood C.R., Collins M.;  RA Henderson S.L., O'Hara R.M. Jr., Turner K.J., Wood C.R., Collins M.;  RA Henderson S.L., O'Hara R.M. Jr., Turner K.J., Wood C.R., Collins M.;  RA Henderson S.L., O'Hara R.M. Jr., Turner K.J., Wood C.R., Collins M.;  RA Sequence FROM N.A.  RC TISSUE-Brain;  RC TISSUE-Brain;  RC TISSUE-Brain;  RC TISSUE-Brain;  RA GUO J., Aplou F., Mellerin M.P., Lebeau B., Jacques Y., Minvielle S.;  RT Chromosome mapping and expression of the human interleukin-13  RT receptor.";  RA GUO J., Aplou F., Mellerin M.P., Lebeau B., Jacques Y., Minvielle S.;  RT GEODNICS 42:141-145(1997).  CC -!- FUNCTION: BINDS AS A MONOMER WITH HIGH AFFINITY TO INTERLEUKIN-13  CC (IL-13), BUT NOT TO IL-4.  CC -!- SUBGELLULAR LOCATION: Type I membrane protein.  CC (IL-13), BUT NOT TO IL-4.  CC -!- SUBGELLULAR COCATION: Type I membrane protein.  CC -!- SUBGELLULAR COCATION: Type I membrane protein.  CC -!- SUBGELLULAR COCATION: Type I membrane protein.  CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.  CC	RESULTATE RESULTION ACCOMMENTATION A	34 112.5 5.3 1631 1 PTP1_DROME P35992 drosophila 35 109.5 5.2 918 1 IL6B_RAY 36 107.5 5.1 638 1 GHR_HUMAN 37 107.5 5.1 837 1 GCSR_MOUSE 39 106 5.0 634 1 GHR_SHEEP 40 105 5.0 511 1 VGLG_VSVO 41 104.5 5.0 1092 1 LIFR_MOUSE 42 102.5 4.9 638 1 GHR_PIG 43 101.5 4.8 638 1 GHR_PIG 44 101.5 4.8 638 1 GHR_RAHT 45 99.5 4.7 507 1 EPOR_MOUSE  ALIGNMENTS  ALIGNMENTS  P35992 drosophila P40190 rattus norv P40191 homo sapien P4023 mus musculu P5100 bos taries Q28575 ovis aries P10484 vesicular s P10756 sus scrofa P13756 sus scrofa Q4 99.5 4.7 507 1 EPOR_MOUSE  ALIGNMENTS
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01-JUL-1993 (Rel. 26, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
Interleukin-5 receptor alpha chain precursor
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Catarrhini; Hominidae;
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Pred. No. 7.8e-166;
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Query Match
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EMBL; M96651; AAA69151.1; ...
EMBL; M95651; AAA36110.1; ...
EMBL; A26249; CAA01793.1; ...
EMBL; A26249; CAA01791.1; ...
EMBL; A26251; CAA01794.1; ...
EMBL; A26251; CAA01794.1; ...
PIR; A40267; A40267.
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DOMAIN
TRANSMEM
                                                                                                                                                                              jenew; nv...
MIN; 147851; ...
InterPro; IPR002996; CR1A.
InterPro; IPR003532; Hemtopoptn_S_F2.
InterPro; PS01356; HEMATOPO_REC_S_F2; 1.
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SEQUENCE FROM N.A.
MEDLINE-92357767; PubMed-1495999;
Throng J., Tuypens T., Plaetin
                                                                                                                                                                                                                                                                                                                                                                                                                                 an IL5-specific alpha chai
for GM-CSF.";
Cell 66:1175-1184(1991).
-!- FUNCTION: THIS IS THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Molecular basis of the membrane-anchored and two the human interleukin 5 receptor alpha subunit."; Proc. Natl. Acad. Sci. U.S.A. 89:7041-7045(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fiers W., Plaetinck G.;
"A human high affinity interleukin-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 1-335 FROM N.A. (S1 F MEDLINE=92005669; PubMed=1833065;
                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Tavernier
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           Similarity
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, Plaetinck
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                                                INTERLEUKIN-5 RECEPTOR ALPHA CHAIN EXTRACELLULAR (POTENTIAL).

POTENTIAL.

CYTOPLASMIC (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

NIDE -> FSR (IN SOLUBLE ISOFORM S1).

MISSING (IN SOLUBLE ISOFORM S2).

MISSING (IN SOLUBLE ISOFORM S2).
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Mismatches
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           310.5;
No. 3.2
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RESULT 3
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AC 009030
DT 01-NOV
DT 16-OCT
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                                                                                                                                                                                                                                                       "Cloning and characterization of a binding subunit of the interleukin 13 receptor that is also a component of the interleukin 4 receptor."; Proc. Natl. Acad. Sci. U.S.A. 93:497-501(1996).

-I. FUNCTION: BINDS IL-13 WITH A LOW AFFINITY. TOGETHER WITH IL-4R-ALPHA CAN FORM A FUNCTIONAL RECEPTOR FOR IL-13. ALSO SERVES AS AN ALPHA CAN FORM PROTEIN TO THE COMMON CYTOKINE RECEPTOR GAMMA CHALN FOR IL-4 SIGNALING, BUT CANNOT REPLACE THE FUNCTION OF GAMMA-C IN ALLOWING ENHANCED IL-2 BINDING ACTIVITY (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Interleukin-13 receptor alpha-1 chain precursor
13RA-1) (Interleukin-13 binding protein) (NR4).
IL13RA1 OR IL13RA OR IL13R.
                                     or send an email
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
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01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                           Willson T.
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=96133964; PubMed=8552669;
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                                                                                                                                           GAMMA-C IN ALLOWING ENHANCED IL-2 BINDING ACTIVITY (BY SIMILARITY).

SUBUNIT: INTERLEUKIN-13 RECEPTOR IS A COMPLEX OF IL4R-ALPHA, IL13R-ALPHA, AND POSSIBLY OTHER COMPONENTS (BY SIMILARITY).

SUBCELLULAR LOCATION: Type I membrane protein.

TISSUE SPECIFICITY: SPLEEN, LIVER, THYMUS, HEART, LUNG, KIDNEY, TESTIS, STOMACH, BRAIN, SKIN, AND COLON: BUT NOT SKELETAL MUSCLE.

SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.

SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
                                                                          European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOUSE
                                                                                                       SWISS-PROT entry is copyright. It is produced through a centre the Swiss Institute of Bioinformatics and the EMBL
MGI:105052;
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            S80963;
                                                                non-profit institutions as long and this statement is not removed.
                                                  requires a license agreement (See http://www.isb-sib.ch/announce/
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            AAB50695.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                      to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                      J.-G., Metcalf D., Alexander W.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chordata;
Rodentia;
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RESULT 4
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                                                                                                                                                                                                                              1131_HUMAN STANDARD; PRT; 427 AA.
P78552; Q99656; O95646;
O1-NOV-1997 (Rel. 35, Created)
O1-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Interleukin-13 receptor alpha-1 chain precursor
13RA-1) (CD213al antigen).
IL13RA1 OR IL13RA OR IL13R.
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TISSUE=Carcinoma;
MEDLINE=97165986; PubMed=9013879;
Miloux B., Laurent P., Bonnin O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
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Mammalia; Eutheria;
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PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
                                                                                        SEQUENCE FROM N.A.
                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                      Homo sapiens (Human)
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             Lupker
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          J., Caput D.,
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             Vita
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Gauchat J.F.M.,
Jeannin P., Alou
Eugster H.P., Bo
Submitted (JAN-1
                                                                                                                                                                                                                                                                                                                                                                                                                        WADA M., HISROT T., KUWANO M.;

SUBMILITED (SEP-1999) to the EMBL/GenBank/DDBJ databases.

SUBMILITED (SEP-1999) to the EMBL/GenBank/DDBJ databases.

SIDMILITED (SEP-1999) to the EMBL/GenBank/DDBJ databases.

ALPHA CAN FORM A FUNCTIONAL RECEPTOR FOR IL-13. ALSO SERVES AS AN ALTERNATE ACCESSORY PROTEIN TO THE COMMON CYTOKINE RECEPTOR GAMMA CHAIN FOR IL-4 SIGNALING, BUT CANNOT REPLACE THE FUNCTION OF GAMMA-C IN ALLOWING ENHANCED IL-2 BINDING ACTIVITY.

SUBUNIT: INTERLEUKIN-13 RECEPTOR IS A COMPLEX OF IL4R-ALPHA, AND POSSIBLY OTHER COMPONENTS.

SUBCELLULAR LOCATION: Type I membrane protein.

TISSUE SPECIFICITY: UBIQUITOUS. HIGHEST LEVELS IN HEART, LIVER, KINEY. ALSO FOUND IN B-CELLS, T-CELLS AND ENDOTHELIAL CELLS.

SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.

SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

DATABASE: NAME-PROW; NOTE-PROW 2:95-100(2001);

WWW-"http://www.ncbi.nlm.nih.gov/prow/guide/435859885_g.htm".
                                                                                                                                                                                                                                                             EMBL; Y10659; CAA71669.1; -. EMBL; Y09328; CAA70508.1; -. EMBL; U62858; AAB37127.1; -. EMBL; U81379; AAD00510.3; -.
    CARBOHYD
                 CARBOHYD
                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-sorsend an email to license@isb-sib.ch).
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Submitted (SEP-1999)
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Aman M.J., Tayebi
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PS01356; HE
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271:29265-29270(1996).
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                                                                                                                                                                                32; Hemtopoptn_S_F2.
   HEMATOPO_REC_S_F2; 1.
mbrane; Glycoprotein; Immunoglobulin
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Biochem. Biophys. F
-!- FUNCTION: THIS
                                                                                                                                              STRAIN=White leghorn; MEDLINE=93075121; Pub!
             between
                                                                                                                                                                                                                Archosauria;
                                                                                                                                                                                                                             Eukaryota; Metazoa;
                                                                                                                                                                                                                                        Gallus
                                                                                                                                                                                                                                                              Prolactin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                        Tanaka M., Maeda K., Okubo T., Nakash
Double antenna structure of chicken
                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                            NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                   PRLR_CHICK
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SUBCELLULAR LOCATION:
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                                            LOCATION: Type I membrane protein.
BELONGS TO THE CYTOKINE FAMILY OF REC
CONTAINS 4 FIBRONECTIN TYPE III-LIKE
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Weognathae; Galliformes; Phasianidae; Phasiani
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            jht. It is produced through a collaboration
Bioinformatics and the EMBL outstation -
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InterPro; IPR003961; FN_III.
InterPro; IPR003528; Hemtopoptn_L_F1
Pfam; PF00041; fn3; 4.
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HSSP; P16471; 1BP3.
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                                                             PFGFI--LILVIFVTGLLLRKPNTYPKMIP
                                                                               QTQYKMFSLNPGKKYI-----IQIHCKPDHHGSWSEWSSENYIQIPNDFRVKDMI-VWI
                                                                                               ET-YTLKTTNETRQLCFVVRSKVNIYCSDD--GIWSEWSDKQCWE-GEDLSKKTLLRFWL
                                                                                                                  DPPVNVTLELKKPINRKPYLVLTWSPPPLADVRSGWLTLEYELRLKPEEGEEWETIFVGQ
                                                                                                                                    LPPVYLTFTRESSCEIK----LKWS-IPLGPIPARCFDYEIEIR----EDDTTLVTATVEN
                                                                                                                                                                      DHALQCVDYIKADGQNIGCRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNIVKP
                                                                                                                                                                                                         QSSWAETTYWISPQG-IPETKVQDMDCVYYNWQYLLCSWKPGIGVLLDTNYNLFYWYEGL
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                                                                                                                                                                                                                                                              TTFNITVTATNEIGSNSSDPQYYDYTSIVQPGSPVNLTLETKRSANIMYLWAKWSPPLLA 156
                                                                                                                                                      EQVYECPDY-RTAGPN-SCYFDKKHTSFWTIYNITVRATNEMGSNSSDPHYVDVTYIVQP
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                                                                                                                                                                                                                                                                                                                                    831 AA;
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 STANDARD;
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26.4%;
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FIBRONECTIN TYPE-III
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Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                          PIR;
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01-MAY-1991 (Rel.
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                                                                                                                                                                                                  SEQUENCE
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InterPro; IPR003532; Hemtopoptn_S_F2.
PROSITE; PS01356; HEMATOPO_REC_S_F2; 1.
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SIMILARITY: BELONGS TO THE CYTOKINE FAMILY O
SIMILARITY: TO IL-13 RECEPTOR ALPHA-2 CHAIN.
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                                                                VTPLHEGFAASVRTILK---SSHTTLASSWVSAEL-KAPPGSPGTSVTNLTCTTHTVVSS
                                                                                GFDLNKGIEAKIHTLLPWQCTNGSEVQSSWAETTYWISPQGIPETKVQDMDCVYYN----
                                                                                                         PPVNFTIKATG-LAQVLLHWDPNPDQEQ-RHVDLEYHVKINAPQEDEYDTRKTES----KC
                                                                                                                              PPQDFEIVDPGYLGYLYLQWQPPLSLDHFKECTVEYELKYRNIGSETWKTIITKNLHYKD
                    HTHLRPYQVSLRCTWLVGKDAPEDTQYFLYYRFGVLTE--KCQEYSRDALNRNTACWFPR
-YLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLPPVYLTFTRESSCEIKLKWS
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                                                                                                                                                                   Similarity
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                                         -WQY-LLCSWKPGIGVLLDTNYNLFYWYEGLDHALQCVDYIK-ADGQNIGCRFP-
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                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  receptor
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ga A., Mita S.,
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24.6%;
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Last annotation update)
r alpha chain precursor
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                                                                                                                                                                                                                                                                                                                                    Glycoprotein;
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                                                                                                                                                                                                                                          POTENTIAL.

CYTOPLASMIC (POTENTIAL).

BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. . . ) (PC
                                                                                                                                                                Score
Pred.
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Sciurognathi; Muridae
                                                                                                                                                                                                   A4326D2922571C08
                                                                                                                                                      Mismatches
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                                                                                                                                                                 247;
No. 5.
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                                                                                                                                                                                                              (GLCNAC
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5.2e-13;
hes 151;
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                                                                                                                                                                                                   CRC64;
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                                                                                                                                                                                                                        (POTENTIAL)
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                                     200
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                                                                                                                                                                                                                                                                                                                                                                                                    Znou J.F., Zadworny D., Guemene D., Kuhn.
"Molecular cloning, tissue distribution,
prolactin receptor during various reproduggallopavo.";
            DOMAIN
TRANSMEM
                                                                                                                                                                                          modified and this statement is not removentities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                    EMBL;
HSSP;
                                                                                                                                                                     EMBL;
                                                                                                                                                                                                                            use
                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                           Pitts G.R., You S.K., Submitted (MAR-1995):
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Archosauria; Aves; Neognathae; NCBI_TaxID=9103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Meleagris gallopavo (Common turkey)
Eukaryota; Metazoa; Chordata; Crani
Archosauria; Aves; Neognathae; Gall
  DOMAIN
                                                                                        InterPro; IPR003528; H
Pfam; PF00041; fn3; 4.
                                                                                                            Interpro; IPR002996; CR1A.
                                                                                                                                                                                                                                                                               -1- SUBCELLULAR LOCATION: Type I membrane protein.
-1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                   Pitts G.
                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Kidney;
MEDLINE-97057891; PubMed-8902221;

""""" D., Guemene D.,
                                              SIGNAL
                                                          Receptor;
                                                                                                                                                                                                                                                                                                                                                            TISSUE-Ovary;
                                                                   PROSITE;
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                                                                                                                                    L76587; AAB01544.1;
U22947; AAA75038.1;
U22924; AAA75039.1;
U22924; ABA75039.1;
P16471; 1BP3.
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                                                                                SM00060;
                                                                   PS01352; HEMATOPO_REC_L_F1;
; Transmembrane;
1 23
24 831
24 438
439 459
460 831
                                                                              FN3;
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                                                                                                    Hemtopoptn_L_F1.
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                                                     Glycoprotein;
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PROLACTIN RECEPTOR.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
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(TPRLR).
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P31785;
01-JUL-1993
01-JUL-1993
15-JUN-2002
Cytokine rec
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CARBOHYD
                               Munakata
"Cloning
                                                                                                                                  Homo
          Science [2]
                                                   SEQUENCE FROM N.A., MEDLINE=92335883; Pareshita T., Asao
                                                                                                Eukaryota; Metazoa; Mammalia; Eutheria; NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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 SEQUENCE
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                    H., Nakamura M., Si
y of the gamma chain
257:379-382(1992).
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1993 (Rel.
2002 (Rel.
2002 (Rel.
2002 (Rel.
  FROM
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                                                      Asao H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA;
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                                                                                                                                                       . 26, Created)
. 26, Last sequence update)
. 41, Last annotation update)
r common gamma chain precurso
chain) (IL-2R gamma chain) (
                                                              PubMed=1631559;
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                                                                                                             Chordata;
Primates;
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26.1%;
                                                     Ohtani K., Ishii N.,
                                Sugamura
in of the
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Pred. No. 6.7e
53; Mismatches
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BY SIMILARITY.
BY SIMILARITY.
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N-LINKED
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Catarrhini;
                                                                                                                                                                                                                            PRT;
                                                                            SEQUENCE.
                                 K.;
human
                                                                                                                                                        precursor (Gamma-C)
chain) (P64) (CD132
                                                                                                                                                                                                                            369
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                                                                                                                         Vertebrata;
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V TYPE-III
V TYPE-III
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.7e-12
                                 IL-2
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                                                                                                              Hominidae;
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                                                      Kumaki S.,
                                receptor.";
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antigen).
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330

390

443

272 178 212

17;

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MEDLINE-94375038; PubMed-8088810; Markiewicz S., Subtil A. Donner de Saint De Carte 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 [8]
VARIANTS
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Structure
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"Sharing of the interleukin-2 (IL-2)
receptors for IL-2 and IL-4.";
Science 262:1874-1877(1993).
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J. Bi
                              MEDLINE=94300093; PubMed=8027558; Ishii N. Asao H. Kimura Y. Takeshita Konno T. Maeda M. Uchiyama T., Sugamur "Impairment of ligand binding and growth receptor gamma-chains in patients with y
                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-94130970; PubMed-829
Disanto J.P., Dautry-Varsat
de Saint Basile G.;
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MEDLINE=94090317; Put
Russell S.M., Kkegan
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Kondo M
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               immunodeficiency
                                                                                                                                                                               "Detection of three nonsense mutations the interleukin-2 receptor gamma chain differently affect the mRNA processing
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                                                                                                                                                                                                                                                                                                                                                     high-affinity
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ferently affect the mRNA
omics 21:291-293(1994).
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INE-95111955; PubMed-7529123;
orough P., Hedgecock C.J., Richar
interleukin-2 and interleukin-4
                                                                                                                                                                                                                                                                                                                                  leukin-2 (IL-2) receptor gamma chain combined immunodeficiency disease reffinity IL-2 receptor binding.";
. Immunol. 24:475-479(1994).
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153:1310-1317(1994).
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PubMed=8266077;
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                                nding and growth signaling of mutant IL-2 patients with X-linked severe combined
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Miyajima A.
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de Saint Basile G.
                                                                                                                                                       morphology.
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immunodeficiency.";
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MEDLINE=96013903;
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Sharfe N., Shahar
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                                                                                                                                                                                                                                                                                                      common gamma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Levinsky R.L., Kinnon C.;
"Screening for mutations
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MEDLINE=95397841;
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SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, I
AND PROBABLY ALSO THE IL-13 RECEPTORS.
SUBCELLULAR LOCATION: Type I membrane protein.
DISEASE: DEFFECTS IN ILZRG ARE THE CAUSE OF A SEVERE COM
IMMUNODEFICIENCY, WHICH IS KNOWN AS AGAMMAGLOBULINEMIA,
OR X-LINKED SEVERE COMBINED IMMUNODEFICIENCY DISEASE (X
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                                                                                                                  INTERLEUKINS
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J.M., Pepper A.E., Bedard P.-M., Laframt ale germ line mosaicism as the origin of a-chain mutation causing X-linked severe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mutational hotspots in the interleukin causing human X-linked severe combined J. Hum. Genet. 57:564-571(1995).
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96:427-432(1995).
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Lester T., Genet S.,
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99:677-680(1997).
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                                                                                                                                 100:3036-3043(1997)
MMON SUBUNIT FOR THE
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M., Roifman C.M.;
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PubMed=7668284;
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SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
DATABASE: NAME-PROW; NOTE-CD guide CD132 entry;
WWW-ncbi.nlm.nih.gov/prow/cd/cd132.htm".
DATABASE: NAME-IL2RGbase; NOTE-X-linked SCID mutation database;
WWW-"http://www.nhgri.nih.gov/DIR/GMBB/SCID/".
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=94283267; PubMed=7516866; Chen X., Horseman N.D.;
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SIMILARITY: BELONGS TO
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LQNIVKPLPPVYLTFTRESSCEIK---
                   LYSKEGEERVYECPDY-KTAGPN-SCYFDKKHTSFWTIYNITVKATNEIGSNVSDPLYVD
                                    FYWYEGLDHALQCVDYIKADGQNIGCRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFQ
                                                        CVLDIGEWSEWSSERHIHIPNGESPPEKPTIIKCRSPEKETFTCWWKPGSDGGHPTNYTL
                                                                           CTNGSEVQSSWAETTYWISPQG-IPETKVQDMDCVYYNWQYLLCSWKPGIGVLLDTNYNL
                                                                                              SPPPLADVTSNSHVYRYELRLKPEEKEEWETV---SVGVQTQYKVNR-LQAGVKYVVQVR
                                                                                                                                     TTYNITVMAMNEIGSNSS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   an email to license@isb-sib.ch).
                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR002996;
IPR003961;
IPR003528;
                                                                                                                                                                                                                                                                                                                                                                                                           Transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expression, and mutational analysis
                                                                                                                                                                                                                830
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FN_III.
                                                                                                                                                                                   10.3%;
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THE CYTOKINE FAMILY OF
                                                                                                                                                                          53;
                                                                                                                                                                                                                                                                                                                                FIBRONECTIN TYPE-III
FIBRONECTIN TYPE-III
FIBRONECTIN TYPE-III
FIBRONECTIN TYPE-III
                                                                                                                                                                                                                                                                                                   FIBRONECTIN TYP
BY SIMILARITY.
BY SIMILARITY.
N-LINKED (GLCNA
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3; Mismatches
                                                                                                                                     -DPQYVDVTSIVQPDAPVNLSLETKTSASTTYLLAKW
                                                                                                                                                                                   Score 216.5;
Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                      POTENTIAL.
CYTOPLASMIC
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                                                                                                                                                                                                                                                                                                                                                                                         EXTRACELLULAR
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-LKWS-IPLGPIPA--RCFDYEIEIREDDTTLV
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                                                                                                                                                SEQUENCE F
STRAIN=B6.
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15-JUN-2002 (Rel. 41, La
Cytokine receptor common
(Interleukin-2 receptor
                                                                                                                         Chiu
                                                                                                                                                                         Eur.
                                                                                                                                                                                                         Disanto J.P., Certain S., Wilson A., Macc
Fischer A., de Saint Basile G.;
"The murine interleukin-2 receptor gamma
                                                             J.
                                                                                                                                                                                    chromosomal localization and expression Eur. J. Immunol. 24:3014-3018(1994).
                                                                                                                                                                                                                                    MEDLINE=95104285; pubMed=7805729; Disanto J.P., Certain S., Wilson A.,
                                                                                                                                                                                                                                                             SEQUENCE FROM
                                                                                                                                                                                                                                                                                    Gene
                                                                                                                                                                                                                                                                                                 gamma
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=93366191; PubMed=8359699;
Kobayashi N., Nakagawa S., Minami Y.,
                                                                                                                                                                                                                                                                                                                                                                                             Cao X., Kozak C.A., Liu Y.J., Noguchi M., O'Connell E., Lee "Characterization of cDNAs encoding the murine interleukin (IL-2R) gamma chain: chromosomal mapping and tissue specif
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN-CBA/CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning of the mouse interleukin 2 receptor gamma demonstration of functional differences between the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=93277575; PubMed=8503926; Kumaki S., Kondo M., Takeshita T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=93277575;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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Mammalia; Eutheria; Rodentia;
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01-FEB-1994
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                                                                                     the
                                                                                                            Dougherty G
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                                                                                                                                    MEDLINE=96341745;
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                                                                                                                                                                                                                                                                                                                                                                                                                                    wedline=93391374; PubMed=8378320;
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                                                                                                Molecular mechanisms regulating
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                                                            e adhesion protein CD44.";
Neurooncol. 26:231-239(1995).
- FUNCTION: COMMON SUBUNIT FOR THE RECEPTORS
INTERLEUKINS.
SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2,
AND PROBABLY ALSO THE IL-13 RECEPTORS.
SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       musculus
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                                                                                                                         R.K.,
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Natl.
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                                                                                                                         Droll A.,
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                                                                                                                       PubMed=8750189;
A., Cooper D.L.,
                                                                                                                                                                                                                                                                                                                                                                         expression."
Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           common
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Last annotation update)
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                                                                                                                                                                                                                                                                                                             of the cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gamma chain) (IL-2R gamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gamma chain precursor (Gamma-C)
gamma chain) (IL-2R gamma chain)
                                                                                                                                                                                                                                                                                                                                                                         90:8464-8468(1993).
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adult
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                                                                                                binding
  RECEPTORS
                                                             A VARIETY
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                                      IL-4,
                                                                                                                                                                                                thymus
                                                                                                                                                                                                             organization
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EMBL; D13765; BAA06279.1; -
EMBL; D13565; BAA02760.1; -
EMBL; L20048; AAA39286.1; -
EMBL; S75852; AAB32904.1; -
EMBL; S75844; AAB32904.1; -
EMBL; S75847; AAB32904.1; -
EMBL; S75847; AAB32904.1; -
EMBL; S75848; AAB32904.1; -
EMBL; S75849; AAB32904.1; -
EMBL; S75849; AAB32904.1; -
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SMART; SM00060; FN3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See or send an email to license@isb-sib.ch).
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InterPro; IPR002996; (
284
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European Bioinformatics Institute
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LERMPPIPP
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                                                                    VRSRYNPICGSSQQWSKWSQPVHWGSHTVEENPSLFALEAVLIPVGTMGLIITLIFVYCW
                                                                                                       VRSKVNIYCSDDGIWSEWSDKQCWEG----EDLSKKTLLRFWLPFGF--ILILVIFVTGL
                                                                                                                                       SESQLELRWK--SRHIKERCLQYLVQYRSNRDRSWTELIVNHEPRFSLPSVDELKRYTFR
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67; Conser
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IPR003531; Hemtopoptn_S_F1
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nbrane; Glycoprotein; Signature  
22 BY SIMILARITY
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No. 3.1e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                         116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Usage
                                                                                                                                                                                                                                                                                                                                                                                                                              CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 and the
                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                         Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                               (POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 bу
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                              (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  restrictions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and
                                                                                                                                                                                                                                                                                                                                                                                           369;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a collaboration - MBL outstation -
                                                                                                                                                                                                                                                                                                                                                        23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for
                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                    283
                                                                                                                                                                                                             165
                                                                                                                                                                                                                                                249
                                                                                                                                                                          307
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RESULT 11
CYRG_CANFA
                                                                                                                                                                                                                                                            Matches
             Best Local
                      Query Match
                                                                                                                 CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cytokine receptor common gamma chain precursor (Gamma-C)
(Interleukin-2 receptor gamma chain) (IL-2R gamma chain) (P64).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Henthorn P.S., Somberg Felsburg P.J.; "IL-2R gamma gene micro
                                                                                                                                                                                                                                                      InterPro; IPR002996; CR1A.
InterPro; IPR003961; FN_III.
InterPro; IPR003531; Hemtopo
SMART; SM00060; FN3; 1.
                                                                                                                                                                                                                                                                                                    EMBL; U04361; AAC48403.1; HSSP; P31785; 1ILM.
                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               severe combined
disease.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Spleen;
MEDLINE=95130114; PubMed=7829104;
                                                                                CARBOHYD
                                                                                           CARBOHYD
                                                                                                       CARBOHYD
                                                                                                                                        DISULFID
                                                                                                                                                    DISULFID
                                                                                                                                                               DOMAIN
                                                                                                                                                                           DOMAIN
                                                                                                                                                                                      TRANSMEM
                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                  Receptor;
                                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                                                                                                                           modified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomics 23:69-74(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Canis familiaris (Dog)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYRG_
                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: THE GAMMA CHAIN IS COMMON TO TH
AND PROBABLY ALSO THE IL-13 RECEPTORS.
SUBCELLULAR LOCATION: Type I membrane pr
DISEASE: DEFECTS IN IL2RG ARE THE CAUSE
                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEVERE COMBINED IMMUNODEFICIENCY.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: COMMON SUBUNIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTERLEUKINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CANFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rg P.J.;
gamma gene microdeletion demonstrates that c
 69;
             Similarity
                                                                                                                                                                                                                                PS01355; HEMATOPO_REC_S_F1; 1.
; Transmembrane; Glycoprotein; Signal.
                                           249
373
                                                                   23
262
262
284
151
151
102
102
159
159
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                    22
373
261
283
373
373
249
249
115
72
115
71
71
75
164
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                                              42516
                                                                                                                                                                                                                                                                                                                                                           institutions as long as atement is not removed. U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata; Craniata; Vertebrata;
           9.98;
                                                                                                                                                                                                                                                                 Hemtopoptn_S_F1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R.L.,
                                              MW.
 48;
                                           N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
N-LINKED (GLCNAC...)
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           Score 208; DB 1;
Pred. No. 7.4e-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fimiani V.M., Puck J.M.,
                                                                                                                                                                        CYTOPLASMIC
                                                                                                                                        POTENTIAL
                                                                                                                                                              FIBRONECTIN
                                                                                                                                                                                               CYTOKINE RECEPTOR COMMON GAMMA CHAIN. EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                      POTENTIAL.
                                                                                                                                                    POTENTIAL
                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi; Fissipedia; Canidae; Canis.
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMMON TO THE IL-2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RECEPTORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               373
                                                                                                                                                                                                                                                                                                                                               (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                               There are no restrictions
                                                                                                                                                              TYPE-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ĀΑ
                                                                                                                                                                        (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein.
 108;
                                                                                                                                                                                                                                                                                                                                                           Usage
                                                                                                                                                                                                                                                                                                                                                                      its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A CANINE X-LINKED
                    Length 373;
                                              CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         canine X-linked f the human
 Indels
                                                                 (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
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                                                         (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                              EMBL
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 40;
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                                                                                                                                                                                                                                                                                                                                                                                                      collaboration
                                                                                                                                                                                                                                                                                                                                                                                             outstation
                                                                                                                                                                                                                                                                                                                                                                       'n
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 Gaps
 12;
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RESULT 12
IL3B_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IL3B_MOUSE
P26954;
01-OCT-1993;
01-OCT-1993;
30-MAY-2000;
                                                                                                                                                                                                                        entities
or send a
                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interleukin-3 receptor class II beta chain precursor (Colony stimulating factor 2 receptor, beta 2 chain).
CSF2RB2 OR AI2CA OR IL3RB2 OR IL3R.
                                                                                                                                                                             PIR;
                            Receptor;
                                                                      Pfam; PF00041; fn3; 2.
SMART; SM00060; FN3; 2
                                                                                                                                                                MGD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=90117145; PubMed=2404337;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; NCBI_TaxID-10090;
                                                      PROSITE; PS01355; HEMATOPO_
                                                                                                                                                                                            EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   receptor gene family.";
Science 247:324-327(1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yahara I.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                   InterPro;
                                                                                                                   InterPro;
                                                                                                                                   InterPro;
                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                     ÷
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Cloning of an interleukin-3 receptor gene: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Itoh N., Yonehara S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31
                                                                                                                                                                                                                                                                                                                                          SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
                                                                                                                                                                                                                                                                                                                                                                                        FUNCTION: IN MOUSE THERE ARE TWO CL
RECEPTORS. ONE CONTAINS THIS IL-3-S
OTHER CONTAINS THE BETA CHAIN ALSO
AND GM-CSF RECEPTORS.
                                                                                             MGI:1339760; Csf2rb2.
rPro; IPR002996; CR1A.
rPro; IPR002982; Cytok_receptor_2.
rPro; IPR003961; FN_III.
rPro; IPR003531; Hemtopoptn_S_F1.
                                                                                                                                                                             M29855; AAA39295.1;
A40091; A40091.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KENPLFASEAVLIPLGSMGLIISLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KKTLL----RFWLPFGFILILVIFV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WDRSWTEQSVDHRNSFSLPSVDGQKFYTFRVRSRYNPLCGSAQRWSEWSHPIHW-GSNTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -DTTLVTATVEN-ETYTLKTTNETRQLCFVVRSKVNIYCSDDGIWSEWSDKQCWEGEDLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --PRRQSTQKLKLQNLVIPWAPENLTLHNLSESQLELSWS---NRHLDHCLEHVVQYRSD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NKPIRSSYFTFQLQNIVKPLPPVYLTFTRESSCEIKLKWSIPLGPIPARCFDYEIEIRED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----TNLTLHYWYKNSNDDKVQECGHYLFSREVTAGCWLQKEEIHLYETFVVQLRDPRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GVLLDTNYNLFYWYEGL--DHALQCVDYIKADGQNIGCRFPYLEASDYKDFYICVNGSSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NGNEDITPDFFLTATPSET --- LSVSSLPLPEVQ --- CFVFNVEYMNCTWNSSSEPRP --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NGSE-----VQSSWAETTYWISPQGIPETKYQDMDCYYYNWQYLLCSW------KPGI 161
                                                                                                                                                                                                                        an email to license@isb-sib.ch).
                                                                                                                                                                                                                                        requires a license agreement
          Transmembrane;
1 22
23 878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arai K., Miyajima
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Rel. 27, Created)
(Rel. 27, Last sequence up)
(Rel. 39, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                          Csf2rb2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chordata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schreurs
                            PO_REC_S_F1; 1.
Glycoprotein; Signal.
POTENTIAL.
            INTERLEUKIN-3 RECEPTOR CLASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 276
                                                                                                                                                                                                                                                                                                                                                                                                    TWO CLASSES OF HIGH-AFFINITY I IL-3-SPECIFIC BETA CHAIN AND IN ALSO SHARED BY HIGH-AFFINITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gorman D.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      878
                                                                                                                                                                                                                                        (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               member of
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              II BETA
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RESULT
CYRG_BO
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Best Local S
Matches 86
                                                                                                                                                                                                                                                                                                                                                                                                                                      CYRG_BOVIN
Q95118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     _BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
DISULFID
DISULFID
DISULFID
DISULFID
CARBOHYD
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cytokine receptor common gamma chain precursor (Gamma-C)
(Interleukin-2 receptor gamma chain) (IL-2R gamma chain)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
TRANSMEM
                               This
                                                                                                                                                 gamma
DNA Ce
 the
                                                                                          -
                                                                                                                                                                                                     SEQUENCE FROM N.A.
MEDLINE=96268473; PubMed=8672241;
YOO J., Stone R.T., Solinas-Todo
                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pebovidae; Bovinae; Bos.
                 between
                                                                                                                      -
                                                                                                                                                                                               LCT
XOO
                                                                                                                                                                                                                                                                      NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                 IL2RG
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                                                                                                                                                                                                loning
                                                    INTERLEUKINS.
SUBUNIT: THE GAMMA CHAIN IS COMMON TO THE IL-2, IL-4, IL AND PROBABLY ALSO THE IL-13 RECEPTORS.
SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
                                                                                                                                             ma gene.";
Cell Biol. 15:453-459(1996).
FUNCTION: COMMON SUBUNIT FOR THE
                                                                                                                                                                                                                                                                                                                                   taurus (Bovine).
   European
SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPQDFEIVDPGYLGYLYLQWQPPL---SLDHFKECTVEYELKYRNIGSETWKTIITKNLH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VRVKPISDY - -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -GCRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLPPVY-LTFTRESSCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -TSNFQVN--LEPKL--FLPNSIYAARVRTRLSAGSSLSGRPSRWSPEVHWDSQPG-DKA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YKDGFDLNKGIEAKIHTLLP------WQCTNGSEVQ---SSWAETTYWISPQGIPET
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POTENTIAL.

CYTOPLASMIC (POTENTIAL).

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entities requires a or send an email to
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InterPro; IPR003531;
YTFRVRSRYNPLCGSAQHWSDWSYPIHW-GSNTSKENIENPENPSLFALEAVLIPLG
                                                                                                                                                                               IPETKVQDMDCVYYNWQYLLCSW-----KPGIGVLLDTNYNLFYWY---EGLDHALQCV
              LCFVVRSKVNIYCSDDGIWSEWSDKQCWEGEDLSKKTLLRFWLPFGFILILVIFVTG
                                                                                                                                                       LPLPKVQ----CFVFNVEYMNCTWNSSSEPQP-----NNLTLHYGYRNFNGDDKLQECG
                                                  LRNLSEFQLELSWS---NRYLDHCLEHLVQYRSDRDRSWTEQSVDHRHSFSLPSVDAQKL
                                                                                                                            DYIKADGQNIGCRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLPPVYLT
                                                                           FTRESSCEIKLKWSIPLGPIPARCFDYEIEIRED-DTTLVTATVEN-ETYTLKTTNETRQ
                                                                                                    HYLFSEGITSGCWFGKKEIRLYETFVVQLQDPREHR--KQPKQMLKLQDLVIPWAPENLT
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                                                                                                                                                                                                       1 Similarity
62; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SM00060;
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CYTOKINE RECEPTOR COMMON G.
EXTRACELLULAR (POTENTIAL).
POTENTIAL.
CYTOPLASMIC (POTENTIAL).
FIBRONECTIN TYPE-III.
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"Molecular cloning of a second subunit of the rece granulocyte-macrophage colony-stimulating factor (reconstitution of a high-affinity GM-CSF receptor. proc. Natl. Acad. Sci. U.S.A. 87:9655-9659(1990).
                                                                                                                                                                                                                                                01-OCT-1993 (Rel.
01-FEB-1996 (Rel.
16-OCT-2001 (Rel.
                                                                              SEQUENCE FROM N.A. MEDLINE=91088571; Hayashida K., Kita
                                                                                                                                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                               Miyajima A.;
"Molecular cloning
                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                    OR IL5RB OR IL3RB.
                                                                                                                                                                                                  (Human)
                                                                                  Kitamura
                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                  PubMed=1702217;
amura T., Gorman
                                                                                                                                                                                                                                  27, Created)
33, Last sequence update)
40, Last annotation update)
common beta chain precursor
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                                                                                                                                                                   Craniata; Vertebrata; Catarrhini; Hominidae
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                                               the receptor
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InterPro; IPR000282; Cytok_r
InterPro; IPR003961; FN_III.
InterPro; IPR003531; Hemtopo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PIR; A39255; A39255.
HSSP; P19235; 1EBA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (FEB-1991)
-!- FUNCTION: HIGH AF
                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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 276 IREDDTTLVTAT-VENETYTLKTTN-----ETRQLCFV-VRSKVNIYCSDDGIWSE
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SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN. THE BE
CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS.
SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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                             PRRAEKHIKSSV-----NI--QMAPPSLNVTKDGD-SYSLRWETMKMRYEHIDHTFEIQ
                                                        GSSENKPIRSSYFTFQLQNIVKPLPPVYLTFTRESSCEIKLKWSIPLGPIPARCFDYEIE
                                                                                     VASSVSFGLFYKPSPDAGEEECSPVLR---EGLGSLHTRHHCQIPVPDPATHGQYIVSVQ
                                                                                                                VLLDTNYNLFYWYEGLDHALQCVDYIKADGQNIG-----CRFPYLEASDYKDFYICVN 215
                                                                                                                                                                         KIHT-LLPWQCTNGSEVQSSWAETTYWISPQGIPETKVQDMDCVYYNWQYLLCSWKPGIG 162
                                                                                                                                                                                                     GSPQSHWLSPGDLEFEVVYKRL-QDSWEDAAILLSNTS----QATLGPEHLMPSSTYVA
                                                                                                                                                                                                                                                            VIPCOSFVVTDVDYFSFQPDRPLGTRLTVTLTQHVQPPEPRDLQISTDQDHFLLTWSVAL
                                                                                                                                            RVRTRLAPGSRLSGR--PSKWSPEVCWDSQPG-DEAQPQNLECFFDGAAVLSCSWEVRKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HGNC:2436; CSF2RB
                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Transmembrane; Glycoprotein; Repeat; Signal 1 16 POTENTIAL.
                                                                                                                                                                                                                                 --KECTVEYELKYRNIGSETWK--TIITKNLHYKDGFDLNKGIE-----A 103
                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                              AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FN3;
                                                                                                                                                                                                                                                                                                                                                                           346
97335

    to the EMBL/GenBank/DDBJ databases.
    AFFINITY RECEPTOR FOR INTERLEUKIN-3, INTERLEUKIN-5

                                                                                                                                                                                                                                                                                                                                                                                                         897
443
460
897
238
434
434
58
191
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                                                                                                                                                                                                                                                                                                                    57; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                    FIBRONECTIN TYP
BY SIMILARITY.
BY SIMILARITY.
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N-LINKED (GLCNAC...) (P
N-LINKED (GLCNAC...) (P
N-LINKED (GLCNAC...) (P
; 3398E37FDB8F393A CRC64;
                                                                                                                                                                                                                                                                                                                                    Pred.
                                                                                                                                                                                                                                                                                                                                                Score 178.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYTOPLASMIC FIBRONECTIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOKINE RECEPTOR COMMON BETA CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXTRACELLULAR (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                   178.5; DB 1;
No. 5.8e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE-III 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL).
                                                                                                                                                                                                                                                                                                                    144;
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                                                                                                                                                                                                                                                                                                                                                  Length 897;
                                                                                                                                                                                                                                                                                                                                                                                                       (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                     Gaps
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CYRB, MACE PROSE ID CYRB, MACE PROSE DT 01-0CT NR NR SEQUEN RX MEDLIN RX RECEPT DRAISM FT DOMAIN FT DOMAIN FT DOMAIN FT CARBOH
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   Matches
                 Query Match
Best Local
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01-OCT-1993
01-OCT-1993
                                                                                                           DISULFID
DISULFID
CARBOHYD
                                                              CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El the European Bioinformatics Institute. There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1993 (Rel. 27, Created)
01-OCT-1993 (Rel. 27, Last sequence up
15-JUN-2002 (Rel. 41, Last annotation
Cytokine receptor common beta chain pr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Cloning and expression of a gene encoding an like protein: identification of another member receptor gene family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

MEDLINE=90319131; PubMed=1695379;

Gorman D.M., Itoh N., Kitamura T.,

Yahara I., Arai K., Miyajima A.;
                                                                                                                                                                                                     TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                          EMBL; M34397; AAA37204.1;
                                                                                                                                                                                                                                                                                                                                                                                                        or send
                                                                                                                                                                                                                                                                                                                                                                                                                                    modified and this statement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- FUNCTION: HIGH AFFINITY RECEPTOR FOR INTERLEUKIN-3, AND GRANULOCYTE-MACROPHAGE COLONY-STIMULATING FACTOR OF AN ALPHA AND A BETA CHAIN. TI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CSF2RB OR CSF2RB1 OR AIC2B OR IL3RB1.
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                                                                                            CARBOHYD
                                                                                                                                                         DOMAIN
                                                                                                                                                                           DOMAIN
                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                                                   Receptor;
                                                                                                                                                                                                                                                                                  PROSITE; PS01355;
                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CHAIN IS COMMON TO THE IL-3, IL-5 AND GM-CSF RECEPTORS
                                                                                                                                                                                                                                                                                                                                             A35782; A35782.
MGI:1339759; Cs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                       an email to license@isb-sib.ch).
                   Similarity
                                                                                                                                                                                                                                                                        IPR002996; CR1A.
IPR000282; Cytok_receptor_2.
IPR003531; Hemtopoptn_S_F1.
PS01355; HEMATOPO_REC_S_F1; 1.
                                                                                                                                                                                                                                                                  Transmembrane;
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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141
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20.7%;
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                                                                                                                                                                                                                                                                  Glycoprotein; Repeat; Signal.
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    69;
Score 173.5;
Pred. No. 1.5e
59; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                     is not removed
                                                            BY SIMILARITY.

BY SIMILARITY.

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

SCE16EDFDC07A999 CRC64;
                                                                                                                                                        CYTOPLASMIC (POTENTIAL). FIBRONECTIN TYPE-III 1. FIBRONECTIN TYPE-III 2.
                                                                                                                                                                                                                                   POTENTIAL.
CYTOKINE RECEPTOR COMMON
                                                                                                                                                                                                      POTENTIAL
                                                                                                                                                                                                                     EXTRACELLULAR (POTENTIAL)
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   57;
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151 FLLEWSVSLGDAQVSWLSSKDIEFEVAYKRL-QDSWEDAYSLHTSKFQVNFEPKLFLPNS 209
                                                                     327 V-----KHLEQGKFIMSYNHIQMEPPTLNLTKNRDS---YSLHWETQKMAYSFIEHTFQ 377
                                                                              214 VNGSSENKPIRSSYFTFOLQNIVKPLPPVYLTFTRESSCEIKLKWSIPLGPIPARCFDYE 273
                                                                                                                                                                                             49 LYLQWQPPL---SLDHFKECTYEYELKYRNIGSETWKTIITKN-----LHYKDGFDLNKG 100
                                                                                                                                                                                                               94 CVPRRCVIPY---TRESITNEDYYSFRPDSDLGIQLMVPLAQNVQPPLPKNVSISSSEDR 150
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Search completed: January 24, 2003, 19:36:39 Job time: 17 secs

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GenCore version 5.1.3 Copyright (c) 1993 - 2003 Compugen Ltd

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Title:
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Maximum DB seq length: 200000000
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                    A_Geneseq_101002:*

1: /SIDSZ/gcgdata/g

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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

### STIMMARTE

Result No.	Score	Query Match I	Length DB	DB	ID	Description
1	2104	100.0	380	18	AAW24972	Human interleukin-
2	2104	100.0	380	18	AAW35295	Human IL-13 bindin
ω	2104	100.0	380	18	AAW36613	Human Zcytor2 cyto
4	2104	100.0	380	19	AAW41520	Human HR-1 recepto
5	2104	100.0	380	19	AAW41502	Human cytokine/pep
σ	2104	100.0	380	19	AAW33603	Homo sapiens HR-1
7	2104	100.0	380	21	AAY95296	IL-13 binding chai
80	2104	100.0	380	22	AAG63812	Amino acid sequenc
9	2104	100.0	380	22	AAY72136	Human interleukin
10	2104	100.0	380	22	AAB29748	Human IL-13 recept

XY PT

New purified human interleukin-13 receptors - and related nucleic acids, useful for diagnosis and treatment of inflammation, allergy,  ${\bf r}$ 

<u>4</u> .	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	11
292	292	292.5	294.5	295.5	295.5	296	297	302.5	305.5	310.5	311.5	311.5	311.5	311.5	456	626.5	935.5	1194.5	1194.5	1194.5	1194.5	1392.5	1392.5	1392.5	1392.5	1392.5	1452.5	1503	1753	1753	1764	1853	2078	2104
13.9	13.9							14.4									44.5																	100.0
335	335	1026	426	427	427	426	313	405	420	421	420	420	396	396	157	145	255	383	383	383	383	565	563	561	561	318	365	386	359	315	317	372	380	380
14	13	16	18	22	18	18	18	22	13	13	19	13	13	13	19	22	22	22	22	21	18	22	22	22	22	22	22	22	19	19	23	18	18	23
AAR33699	AAR25063	AAR70121	AAW09822	AAB19807	AAW24973	AAW09821	AAW21856	AAU69132	AAR22215	AAR25064	AAW82842	AAR22219	AAR22220	AAR22216	AAW56252	AAU69133	AAU69134	AAB29747	AAY72135	AAY95295	AAW35294	AAU69139	AAU69140	AAU69141	AAU69138	AAU69137	AAU69136	AAU69135	AAW56260	AAW56261	AAE13746	AAW36616	AAW36614	AAM49201
shIL-5R-alpha. Sy	ble human	IL5-R-GBP 130 fusi				Mouse interleukin-	Protein used in pr	Canine interleukin	Sequence of human	Human IL-5 recepto	_	Sequence of secret	Sequence of secret	Sequence of human	Interleukin-13 bin	Canine interleukin	e inter	Mouse IL-13 recept	Murine interleukin	IL-13 binding chai								Canine interleukin		Mature interleukin		us macaq	Zcytor2	Human IL-13R alpha

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WPI; 1997-319773/29. N-PSDB; AAT85826, AAT86464.		Caput D, Ferrara P, Laurent P, Vita N;		(SNFI ) SANOFI SA.		06-DEC-1995; 95FR-0014424.		07-NOV-1996; 96WO-FR01756.		12-JUN-1997.		WO9720926-A1.		Homo sapiens.		<pre>Interleukin-13 receptor; diagnosis; inflammation; allergy; IL-13.</pre>		Human interleukin-13 beta receptor.		22-JUN-1998 (first entry)		AAW24972;		AAW24972 standard; protein; 380 AA.	AAW24972	LT 1

 $\mathbf{v} \times \mathbf{consons}$ 

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AAW3529
ID AAW3529
ID AAW37
XX AAW3
XX AAW3
XX DT 27-M
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KW medik
XX inte
XX alle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cc and 427 as proteins are designated IL-I3R beta and alpha respectively.

Cc The IL-I3R beta has high affinity for IL-I3 while IL-I3R alpha has low affinity, but acquires high affinity when associated with the IL-4 creeptor. Nucleic acids encoding IL-I3R beta and alpha are used as Cc diagnostic probes to identify aberrant synthesis or genetic anomalies could be so identify aberrant synthesis or genetic anomalies of heterozygosity and rearrangements, or chromosomal cc anomalies. They are also used for production of recombinant IL-I3R beta can dalpha which can be used as IL-I3 antagonists, specifically to regulate IL-I3-induced responses for treatment of inflammation and cc allergy. II-I3 receptors are also useful as antisense molecules for gene therapy (blocking synthesis of IL-I3R). Antibodies are used (in standard cc immunoassays) to diagnose diseases associated with abnormal expression cc of IL-I3 receptors; when coupled to a toxin also for treatment of used to identify ligands and modulators of IL-I3R. Note: IL-I3R beta is encoded by the nucleic acid sequence shown in Figure 2a in the sequence light (AAR786464), which is not the same as that shown in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local
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                    allergy; asthma;
                                     mediator; IL-13 receptor binding inhibition; IgE-mediated condition;
                                                        Interleukin-13;
                                                                                          Human IL-13 binding chain of the IL-13 receptor
                                                                                                                               27-MAR-1998
                                                                                                                                                                                                     AAW35295 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
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                                                                                                                                                                                                                                                                                                                LLLRKPNTYPKMIPEFFCDT
                                                                                                                                                                                                                                                                                                                                                                                      TRQLCFVVRSKVNIYCSDDGIWSEWSDKQCWEGEDLSKKTLLRFWLPFGFILILVIFVTG
                                                                                                                                                                                                                                                                                                                                                                                                                                     SSWAETTYWISPQGIPETKVQDMDCVYYNWQYLLCSWKPGIGVLLDTNYNLFYWYEGLDH 180
                                                                                                                                                                                                                                                                                             LLLRKPNTYPKMIPEFFCDT 380
                                                                                                                                                                                                                                                                                                                                                                   TRQLCFVVRSKVNIYCSDDGIWSEWSDKQCWEGEDLSKKTLLRFWLPFGFILILVIFVTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALQCVDYIKADGQNIGCREPYLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MAFVCLAIGCLYTFLISTTFGCTSSSDTEIKVNPPQDFEIVDPGYLGYLYLQWQPPLSLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SSWAETTYWISPQGIPETKVQDMDCVYYNWQYLLCSWKPGIGVLLDTNYNLFYWYEGLDH
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                                                                                                                            (first entry)
                                                      IL-13; interleukin-13 receptor binding chain; IL-13bc;
                    immune complex disorder
                                                                                                                                                                                                     Protein; 380
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Pred. No. 2e-197;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                            mediator of the known biological activities of IL-13. Recombinant IL-13bc proteins, and antibodies raised against them, are used to inhibit the binding of IL-13 to its receptor. They are particularly used to treat IgE-mediated conditions, e.g. allergy, asthma and immune complex disorders, especially lupus, nephritis, thyroiditis and Grave's disease. They are also used to treat immune deficiency (particularly in haematopoietic progenitor cells), cancer etc., and to increase macrophage activation, e.g. in vaccination. To potentiate IL-13 activity, a protein with such activity is combined with IL-13bc and the mixture applied, in vivo, to a cell expressing at least one chain of the IL-13 receptor other than IL-13bc. IL-13bc can also be used in diagnosis to detect expression of IL-13, its receptor or binding chain, and to raise specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid encoding interleukin-13 receptor binding chain and transformed cells - proteins, antibodies and inhibitors, for treating immunoglobulin E-mediated diseases, e.g. Graves disease. and in diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Key
Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The
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                                                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present sequence represents the human interleukin-13 (IL-13) binding in of the interleukin-13 receptor, designated IL-13bc. IL-13bc acts a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ç
                                                                                                                                                                                SSWAETTYWISPQGIPETKVQDMDCVYYNWQYLLCSWKPGIGVLLDTNYNLFYWYEGLDH
                                                                                                         ALQCVDYIKADGQNIGCRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLP
                                     SSWAETTYWISPQGIPETKVQDMDCVYYNWQYLLCSWKPGIGVLLDTNYNLFYWYEGLDH
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                                                                                                                                                                                                                                                        Conservative
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1..25
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/note= "putative"
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                                                                                                                                                                                                                                                                                                                                                               be useful for treating some tumours.
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                                                                                                                                                                                                                                                    Score 2104; DB 18; pred. No. 2e-197; or amatches 0;
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which shares homology with cytokine receptors and was isolated from human placental polyA+ RNA. The resulting polypetide is a receptor for cytokines (particularly interleukin-13) and is expressed on the surface of testicular cells, probably being involved in spermatogenesis. It can be used to detect ligands that promote proliferation and/or differentiation of such cells in cultures and may also be used to treat infertility. Antagonists of this receptor may be used to characterise ligand receptor interactions and as male-specific contraceptives. By blocking the action of IL-13, receptor antagonists and ligand-binding this receptor can also be used to modulate immune function, e.g. in allergy and asthma, as a diagnostic to determine circulation
                                                                                                                                                                                                                                          Claim 2;
                                                                                                                                                                                                                                                                         New nucleic acid encoding testis-specific cytokine receptor - use for identification of ligands or antagonists, potentially for use male contraceptives or for infertility treatment
                                                                                                                                                                                                                                                                                                                                                  WPI; 1997-470820/43.
N-PSDB; AAT96782.
                                                                                                                                                                                                                                                                                                                                                                                                    Baumgartner
O'Hara PJ;
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                                                                                                                                                                                                                                      Page 47-48; 79pp;
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therapeutic.
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use as
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                                          (HUMA-) HUMAN GENOME SCI INC. (SMIK ) SMITHKLINE BEECHAM CO
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ligand and also to isolate and purify ligands. Antibodies can be used assay circulating receptor (an abnormal level may be indicative of disease such as cancer), for labelling cells that express the receptor and therapeutically as antagonist.
                   LLLRKPNTYPKMIPEFFCDT
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Pred. No. 2e-197;
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AAW41520 standard; 12-JUN-1996; 18-DEC-1997 WO9747741-A1 haematopoietic 22-JUN-1998 AAW41520; sapiens receptor; HR-1 receptor. (first 96WO-US10262 disorder; human; /label= 22..380 Location/Qualifiers /label= Protein; entry) cytokine; infection; asthma; allergy; Sig\_peptide Mat\_protein tumour; 380 À therapy; diagnosis

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96WO-US10262

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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This protein comprises a novel human cytokine/peptide hormone creeptor, designated the HR-1 receptor, that shows 27% identity and 52% similarity to the interleukin-5 receptor. Its amino acid sequence was deduced from a cDNA clone (see AAV04131) obtained from a chaimed method for identifying in claimed host cells, and used in a claimed method for identifying compounds which bind to, and activate or inhibit, it. HR-1 receptor activators and agonists can be used to treat, prevent or diagnose predisposition to lowered resistance to infection, asthma, allergic or haemacopoietic disorders, e.g. where induced by AIDS, aplastic anaemia, neutropaenia or cytotoxic treatments for cancer. HR-1 antagonists, e.g. antibodies or HR-1 receptor fragments, can be used to treat conditions associated with HR-1 receptor creeptor. The antibodies can also be used to determine HR-1 receptor levels, since overexpression may be diagnostic of tumours.
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Best Local S
Matches 380
HR-1 receptor; cytokine receptor;
infection; burn; trauma; asthma; a
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                                    Human cytokine/peptide receptor, HR-1 receptor.
                                                                                                                 AAW41502 standard; Protein;
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DB; AAV04131.
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; peptide hormone receptor; human;
allergy; AIDS; aplastic anaemia;
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receptor, designated HR-1 receptor. The amino acid sequence was deduced from a cDNA clone (see AAVO4075) isolated from a human test test is cDNA library. It shows 27% amino acid identity and 52% similarity with the human interleukin-5 receptor. Also claimed are polynucleotides encoding HR-1 receptor, vector and host cells, an agonist to the polypeptide, antibody against the polypeptide, an atlagonist that inhibits the activity of the polypeptide, an antagonist that inhibits the activity of the polypeptide, a process for diagnosing a disease, or a susceptibility to disease, related to expression of HR-1 receptor, and a method for identifying compounds that activate or inhibit the HR-1 receptor. HR-1 receptor protein and polynucleotides can be used for research, biological, diagnosis and (gene) therapy applications, e.g. to increase resistance to infections in individuals with trauma and/or burns, and to prevent, ameliorate, treat, diagnose and/or determine predisposition to asthma, allergic disorders or disorders of cyclic neutropaenia or as a consequence of cytotoxic therapy of cancer, lymphoma, leukaemia and/or bone marrow transplantation.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
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/note= "Claim 14"
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Pred. No. 2e-197;
Mismatches (
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Peptide
                                                                                                                                                                        DNA encoding human cytokine-peptide hormone receptor - use treating preventing or diagnosing, e.g. lowered resistance infection, asthma, allergy, or haematopoietic disease
                   receptor, e.g. antibodies or fragments of it may be used to treat conditions associated with overexpression of the HR-1 receptor, e.g. those listed above. Antibodies may also be used to assay levels of HR-1 receptor, overexpression of which may be diagnostic of tumours, by usual immunoassays; to isolate and identify HR-1 receptor-expressing cells; or for affinity purification of the HR-1 receptor.
                                                                              The sequence is that of the human cytokine/peptide hormone receptor (HR-1 receptor). This, or it's activators or agonists, can be used to treat, prevent or diagnose predisposition to lowered resistance to infection, asthma, allergic or haematopoietic disorders, e.g. where induced by acquired immune deficiency syndrome (AIDS), aplastic anaemia, neutropaenia or cytotoxic treatments for cancer. Antagonists of the
                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo
                                                                                                                                                                                                                                                                      (HUMA-)
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 Sequence
                  immunoassays; to isolate of affinity purification
                                                                                                                                                        Claim 15; Fig 1; 75pp; English.
                                                                                                                                                                                                                    N-PSDB;
                                                                                                                                                                                                                                                  Appelbaum ER,
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12-JUN-1996;
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SMITHKLINE BEECHAM CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                             allergic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         hormone receptor; AIDS; acquired immune deficienc aplastic anaemia; neutropaenia; cancer treatment; resistance; diagnosis; tumours; HR-1 receptor; llergic; haematopoietic; disorder.
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13-DEC-1999;
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                                       WO200036103-A1
                                                                                          Domain
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99WO-US29493.
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                             Interleukin-13 receptor; IL-13 binding chain; IL-13bc; mouse; cytokine receptor; haematopoletin receptor; atopy; allergy; asthma; immune complex disease; lupus; nephritis; thyroiditis; Grave's disease; inflammatory; infection; therapy; antiallergic;
                                                                                                                                                                                                                                                                                                              antiinflammatory; antiasthmatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MAFVCLAIGCLYTELISTTEGCTSSSDTEIKVNPPQDFEIVDPGYLGYLYLQWQPPLSLD
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                                                                                                                                                                                                                                                                                                                                                                                                                  binding chain of human IL-13 receptor.
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26..34]
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                                                                                                                                                                        "mature protein"
                                                                                                                                                                                                        "signal
                                                                    "transmembrane
                                                                                                                                      "extracellular domain; a polypeptide
"intracellular domain; a polypeptide comprising amino acids 257-383 is specifically claimed in Claim 11(f)
                                                                                                      specifically claimed
                                                                                                                    comprising amino acids 22-334
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Pred. No. 2e-197;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             diseases including atopy, allergy, asthma, immune complex diseases (e.g. lupus, nephrotic syndrome, nephritis, glomerulonephritis, thyroiditis and Grave's disease), lung inflammation, immunodeficiency, and cancer. Since IL-13 inhibits macrophage activation, IL-13bc proteins can also be used to enhance macrophage activation, e.g. in vaccination, treatment of mycobacterial or intracellular organisms or parasite infections. IL-13bc proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11(d); Page 53-54;
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Pred. No. 2e-197;
Pred. No. 2e-197;
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Stimulating immune response against interleukin-13 receptor alpha2 subunit in a subject having or at risk of developing gliomas, invocormulating a vaccine comprising an agent that stimulates immune
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                                                                          Claim la; Page 69-70; 72pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human interleukin (IL)-13 binding chain of IL-13 receptor (IL13bc).
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    invention relates to a method of treating, or inhibiting formation of tissue fibrosis in mammals, which involves
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342..362
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as yg99f10.rl human cDNA clone 41648 5"
26. 380
/label= Mature_human_interleukin (IL)-13_binding_chain_
of_IL-13_receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "This region is identical to the translated sequence of an expressed sequence tag (EST) identical as yg99fl0.rl human cDNA clone 41648 5"
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                                                                                                                                                                                                              Human; IL-13 receptor; interleukin-13; IL-13 binding chain;
IL-13bc; IL-13 antagonist; fibrosis inhibition; scarring; v
                                                                                                                                                                                                                                                                                        Human
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB29748
                                                                                                                                                                 wound healing; schistosoma cartilage; cardiac tissue;
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                                                                                                                                                intestinal tissue;
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                                                                                                                                                                                                                                                                                        IL-13
                                                                                                                                                                                                                                                                                                                                                                                                                                   standard; Protein;
                                                                                                                                                                                                                                                                                   receptor IL-13 binding chain (IL-13bc).
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vascular tissue;

infection; liver; skin; muscle; lung tissue; uterine tissue;

vulnerary;

neural tissue

380

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administering a pharmaceutical composition comprising interleukin (IL)-13 antagonist. The protein of the invention is useful for treating tissue fibrosis resulting from infection with Schistosoma or from healing of a wound which is a surgical incision, or inhibiting formation of tissue fibrosis which affects tissues such as liver, skin epidermis and endodermis, muscle, tendon, cartilage, cardiac tissue, pancreas, lung, uterine tissue, neural tissue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of various II-13 related conditions such as allergic conditions, nephrotic syndrome, thyroiditis, Grave's disease and cancer. The present sequence is human interleukin (II)-13 binding chain of II-13 receptor (II-13b). II-13bc protein is used to potentiate the effects of II-13. This protein is also used to enhance macrophage activation and hence can be used in vaccination or treatment of mycobacterial or parasitic infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             testis, ovary, adrenal gland, artery, vein, colon, small ir billary tract and gut. It is also used in the treatment or
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                                                          RESULT 11
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Best Local S
Matches 380
  AAM49201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a method of treating fibrosis in a mammal by administering an interleukin-13 (IL-13) antagonist or an IL-4 antagonist. In particular, the IL-13 antagonist is the IL-13 binding chain (IL-13bc; AAB29747, AAB29748) of the IL-13 receptor (IL-13R), or soluble fragments thereof. The method is useful for treating or inhibiting the formation of tissue fibrosis resulting from the healing of a wound, including a surgical incision wound, or from infection with schiscosoma. The method may be used to treat fibrosis in a variety of tissues, particularly liver tissue, but also skin epidermis, skin
                              AAM49201 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Treating or inhibiting tissue fibrosis resulting from infection with schistosoma and wound healing involves administering interleukin-13 or interleukin-4 antagonist -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                adrenal gland, artery, vein, colon, small inte
tissue. The present sequence represents human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          tissue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          endodermis, muscle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; Page 76-77; 82pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28-APR-2000;
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DB; AAC81416.
                                                                                                 LLLRKPNTYPKMIPEFFCDT
                                                                                                                                                                     TRQLCFVVRSKVNIYCSDDGIWSEWSDKQCWEGEDLSKKTLLRFWLPFGFILILVIFVTG
                                                                                                                                                                                                                            PVYLTFTRESSCEIKLKWSIPLGPIPARCFDYEIEIREDDTTLVTATVENETYTLKTTNE
                                                                                                                                                                                                                                                                                     ALQCVDYIKADGQNIGCRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLP
                                                                                                                                                                                                                                                                                                                                          SSWAETTYWISPQGIPETKVQDMDCVYYNWQYLLCSWKPGIGVLLDTNYNLFYWYEGLDH 180
                                                                                                                             LLLRKPNTYPKMIPEFFCDT
                                                                                                                                                      TRQLCFVVRSKVNIYCSDDGIWSEWSDKQCWEGEDLSKKTLLRFWLPFGFILILVIFVTG
                                                                                                                                                                                                               PVYLTFTRESSCEIKLKWSIPLGPIPARCFDYEIEIREDDTTLVTATVENETYTLKTTNE
                                                                                                                                                                                                                                                                     ALQCVDYIKADGQNIGCRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLP
                                                                                                                                                                                                                                                                                                                             SSWAETTYWISPQGIPETKVQDMDCVYYNWQYLLCSWKPGIGVLLDTNYNLFYWYEGLDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 380;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mis, muscle, tendon, cartilage, cardiac tissue, pancreatic lung tissue, uterine tissue, neural tissue, testis, ovary, gland, artery, vein, colon, small intestine, biliary tract
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENETICS INST INC
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MJ, Wood C;
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                             Protein; 380
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Pred.
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matches 0;
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The invention relates to the use of a nucleic acid or vector CC encoding a polypeptide with at least 70% identity to interleukin-13 CC receptor alpha-2 chain (IL-13R alpha-2; AAM49201) for rendering a CC cancer cell sensitive to IL-3R-targeted immunoconjugates or for CC inhibiting the growth of a cancer cell. In some cancers that exhibit CC little or no expression of IL-13R transfection with the IL-13R CC alpha-2 chain is sufficient to inhibit growth, while in CC other such cancers, the introduction of the IL-13R alpha-2 chain enables immunoconjugates (such as immunotoxins) that comprise IL-13 to be CC in the inhibition or death of cells in the invention also results (CC in the inhibition or death of cells in the tumour which were not CC in the inhibition of at least some of the cells of a tumour with the IL-13R alpha-2 chain causes the secretion of a cytokine or other factor that CC alpha-2 chain causes the secretion of a cytokine or other factor that CC alpha-2 chain activated to kill the tumour cells. Because a nucleic acid encoding just the IL-13R alpha-2 chain is used, rather than a much larger CC uncleic acid encoding the multiple chains of the entire IL-13R, the CC choice of vectors that can be used for transfection. A wide range of CC cancers can be treated using the methods of the invention, including CC brain cancer, head and neck cancer (preferably sequamous cell carcinoma), breast cancer, postate cancer, lung cancer, mesothelioma, pancreatic cancer, colon cancer, gastric cancer, ovarian cancer, renal cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Use of nucleic acid or vector encoding interleukin-13 receptor alpha chain polypeptide that binds IL-13, for sensitizing a cancer cell e.g brain cancer cell to effector molecule or inhibiting growth of cancer
                                                                                                                        bladder cancer, prostate cancer, testicular cancer, skin cancer, cancer, uterine cancer, or sarcoma. The present sequence represent the human IL-13R alpha-2 chain which is specifically claimed for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mesothelioma; pancreatic; colon; gastric; ovarian; renal; bladder; prostate; testicular; skin; cervical; uterine; sarcoma; cytostatic;
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB;
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                                                                                  Note: The present sequence is not shown in the specification,
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                                                                                                     use in
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DB; ABL55245.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; IL-13R alpha-2 chain; interleukin-13 receptor; sensitisation; immunoconjugate; immunotoxin; growth inhibition; cancer; tumou, head and neck; squamous cell carcinoma; breast; liver; lung;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Page -; 80pp; English
                                                                                                     man IL-13R alpha-2 chain which is the method of the invention.
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  380
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                                                                                                                                            present sequence represents
                                                            (X95302) referred to
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Query Match Best Local Si Matches 380;

Similarity

100.0%; 100.0%; tive 0;

Score 2104; DB 23; Pred. No. 2e-197;

Mismatches

0

Length Indels

Gaps

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380;

Conservative

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*RESULT 12
AAW36614
ID AAW36
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AC AAW36
AC AAW36
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DT 30-MA
XX
DT WINTER
XX
LE Humar
XX
KW Cytol
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shares homology with cytokine receptors and was isolated from a human testis cDNA library. The resulting polypeptide is a receptor for cytokines (particularly interleukin-13) and is expressed on the surface of testicular cells, probably being involved in spermatogenesis. It can be used to detect ligands that promote proliferation and/or
                                                                                                                                                                                      male
                                                                                                                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                                                          Baumgartner
O'Hara PJ;
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                                                                                                                                               Claim
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                                                                                                                                                                                nucleic acid encoding testis-specific cytokine receptor - identification of ligands or antagonists, potentially for e contraceptives or for infertility treatment
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MAFVCLAIGCLYTFLISTTFGCTSSSDTEIKVNPPQDFEIVDPGYLGYLYLQWQPPLSLD
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                                                                                                                                               1; Page 51-53;
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use as
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XX Celek
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                                                                                                                                                                                                      Key
Protein
                                                                                                                                                                                                                                                                                                                                                            Celebus
          13-MAR-1996;
                                                                                     18-SEP-1997
                                                                                                                           WO9733913-A1
                                                                                                                                                                                                                                                               Macaque
                                                                                                                                                                                                                                                                                                                      Cytokine
                                              12-MAR-1997;
                                                                                                                                                                                                                                                                                                 infertility;
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sp.

/label= /note=

"partial Zcytor2

protein

sequence"

Location/Qualifiers

96US-0013345 97WO-US04043. macaque

Zcytor2

protein

receptor; ligand binding; testicular cell; ity; antagonist; contraceptive; diagnostic;

spermatogenesis; therapeutic.

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Best Local S
Matches 377
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 30-MAR-1998
                             AAW36616;
                                                     AAW36616 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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377; Conservative
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(first entry)
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                                                       Protein;
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Pred. No. 6.9e-195;
0; Mismatches 3;
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                                                                                     AAE13746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      spermatogenesis. It can be used to detect ligands promoting proliferation and/or differentiation of such cells in cultures and may also be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O'Hara
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              is a
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for identification of ligands or antagonists, potentially for
male contraceptives or for infertility treatment
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                                                                                                                                                                                                                                                                                                                                                                          TRQLCFVVRSKVNIYCSDDGIWSEWSDKQCWEGEDLSKKTLLRFWLPFGFILILVIFVTG
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DB; AAT96784.
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Pred. No. 7.4e-173;
7; Mismatches 22;
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                                                                                                                                                                                                                                                                                                                                                                            CC The invention relates to an isolated soluble zalphall cytokine receptor CC polypeptide and their cDNA molecules. Zalpha proteins are useful for CC inhibiting or antagonising the ligand activity-induced proliferation of CC haematopoietic cells and haematopoietic cell progenitors preferably CC Zalpha is useful for treating immune and inflammatory disorders, for CC Zalpha is useful for treating immune and inflammatory disorders, for CC Zalpha is useful for treating immune and inflammatory disorders. Zalpha is CC immune response in a mammal exposed to an antigen or pathogen. Zalpha is CC useful for treating diseases that require immune regulation including CC autoinmune diseases such as rheumatoid arthritis, multiple sclerosis, CC myasthenia gravis, systemic lupus erythematosus (SLE) and diabetes; CC asptina, ulcerative colitis, inflammatory bowel disease, Crohn's disease, CS espais, viral infection (dengue virus infection) and cancer. The present CC sepais, viral infection (dengue virus infection) and cancer. The present CC sepais, viral infection (dengue virus infection) and cancer. The present CC sepais in the color of the invention.
                                                                                                                                                                                                                                                                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel soluble receptor polypeptides and polynucleotides used cytokine antagonist for stimulating ligand activity-induced proliferation of hematopoletic cells and for suppressing immuresponse in a mammal
                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 240-241;
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28-JUL-2000;
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YKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLPPVYLTFTRESSCEIKLKWSIPLGPIP
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                                     YKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLPPVYLTFTRESSCEIKLKWSIPLGPIP
                                                                    YYNWQYLLCSWKPGIGVLLDTNYNLFYWYEGLDHALQCVDYIKADGQNIGCRFPYLEASD
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Pred. No. 3.1e-164;
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Best Local Similarity
Matches 315; Conserv
                                                                                                                                                                                                                          The II-13 binding protein and related therapeutic molecules can be used in the antagonism of at least one II-13 activity. They can be used for treating II-13 mediated conditions such as certain allergic conditions such as asthma or to inactivate locally administered II-13 after II-13 treatment. The products can also be used as diagnostic agents, e.g. for detecting autoimmune diseases. The antibodies can also be used for immunotherapy and may also be used as a diagnostic tool.
                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-207062/18.
N-PSDB; AAV22702.
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10-SEP-1996;
                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                             Disclosure; Page 55-56; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                      New isolated interleukin-13 binding protein - used to develop products for therapy e.g. for allergic conditions such as asthma or for diagnosis or detection {\sf Conditions}
                                                                                                                                                                                                                                                                                                                                                                                                                                              Hilton DJ, Nicola NA,
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NWQYLLCSWKPGIGVLLDTNYNLFYWYEGLDHALQCVDYIKADGQNIGCRFPYLEASDYK 208
                                                 EIKVNPPQDFEIVDPGYLGYLYLQWQPPLSLDHFKECTVEYELKYRNIGSETWKTIITKN 88
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isease; antibody; immunotherapy.
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Search completed: January 24, 2003, Job time: 38 secs

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Copyright (c) 1993 - 2003 Compugen
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Q920b8 rattus norv
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222 10.6 368 6 Q8SQ71 212.5 10.1 278 11 Q9LBF6 187 8.9 611 13 Q9LBF6 187 8.9 611 13 Q9LBF6 188.9 611 13 Q9LBF6 178.5 8.8 834 13 Q9LBC01 178.8 8.5 896 11 Q6QZX9 174.5 8.3 896 11 Q6QZX9 177.5 8.3 896 11 Q9ZX9 177.6 8.1 890 11 Q9ZX9 177.7 8.1 890 11 Q9ZX9 177.7 8.1 890 11 Q9ZX9 178.7 7.9 622 6 Q9NOJ7 186.7 7.9 626 13 Q9QGX9 185.5 7.4 625 6 Q9XS92 185.7 7.4 625 6 Q9XS92 185.7 7.4 626 13 Q9OWG7 185.7 7.2 208 4 Q9CBJ8 185.7 7.2 208 4 Q9CBJ8 185.7 7.2 208 4 Q9CBJ8 185.7 7.0 538 13 Q9GBJ9 186.5 7.0 422 4 Q9UHH5 187.5 7.0 538 13 Q9UBH5 188.5 6.8 425 11 Q9JWS9 198.6 6.9 425 4 Q9UBH7 198.7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7 7			13	346		135	44
222 10.6 368 6 Q8SQ71 Q8Sq71 s 212.5 10.1 278 11 Q9UHR8 Q9ibf6 1187 8.9 611 13 Q9IBF6 Q9ibf6 1187 8.9 611 13 Q9IBF6 Q9ibf6 1185.5 8.8 84 13 Q9DEQ1 Q9dEq1 178.5 8.8 896 11 Q8QZX9 177.5 8.3 896 11 Q8QZX9 177.5 8.3 896 11 Q9ZX9 Q9th9 173.5 8.3 881 13 Q9PH9 Q9th9 173.5 8.2 881 13 Q9PH9 Q9ZX9 170 8.1 890 11 Q9ZX9 Q9ZX9 170 8.1 890 11 Q9ZX9 Q9ZX9 170 8.1 890 11 Q9ZX9 Q9ZX9 Q9ZX9 175 6 608 11 Q9ZX9 Q9ZX9 Q9ZX9 Q9ZX9 175 7.4 625 6 Q9XS92 Q9ZX9 Q9ZX9 175 7.4 625 6 Q9XS92 Q9ZX9 Q9ZX9 175 7.4 625 6 Q9XS92 Q9ZX9 Q9ZX Q9ZX	homo	_	4	390		138	43
222 10.6 368 6 Q8SQ71 Q8Sq71 s 212.5 10.1 278 11 Q9IBF6 Q9ibf6 11 3 Q9IBF6 Q9ibf6 Q9ibf6 11 3 Q9IBF6 Q9ibf6 Q9ibf6 11 3 Q9IBF6 Q9ibf6 Q9ibf6 11 0 Q9IBF0 Q9ibf6 Q9ibf6 175.5 8.3 896 11 Q64146 Q9ibf6 Q9ibf6 175.5 8.3 896 11 Q8ZX9 Q9ibf9 Q9ibf	mus		11	425		•	
222 10.6 368 6 Q8SQ71 Q8Sq71 s 212.5 10.1 278 11 Q9LBF6 187 8.9 611 13 Q9LBF6 187 8.8 8.5 896 11 Q6QLX9 Q8qLY9 Q8qLY9 Q8qLY9 Q8qLY9 Q8qLY9 Q9LH9 173.5 8.3 896 11 Q9LLA0 Q8qLY9 Q9LH9 173.5 8.3 811 13 Q9LLA0 Q	homo	0	4	422			
222 10.6 368 6 Q8SQ71 Q8Sq71 s 212.5 10.1 278 11 Q9IFR8 Q9ibf6 187 8.9 611 13 Q9IFF6 Q9ibf6 187 8.9 611 13 Q9IFF0 Q9ibf6 185.5 8.8 343 13 Q9IFG1 Q9ibf6 175.5 8.3 896 11 Q8QZX9 174.5 8.3 896 11 Q8QZX9 174.5 8.3 881 13 Q9FFH9 Q9ibf0 Q9ibf0 173.5 8.2 881 13 Q9FFH9 Q9ibf0	ъ	_	4	422		•	40
222 10.6 368 6 Q8SQ71 222 10.6 368 6 Q8SQ71 212.5 10.1 278 11 Q9IBF8 187 8.9 611 13 Q9IBF8 188 9 611 13 Q9IBF8 198 1 13 Q9IBF8 198 8.5 896 11 Q9IBG1 175.5 8.3 896 11 Q8DZX9 174.5 8.3 896 11 Q9ZX9 177.5 8.2 881 13 Q9PFH9 173.5 8.2 881 13 Q9PFH9 173.5 8.2 881 13 Q9PFH9 175.6 6.3 611 13 Q9PFH9 176.7 7.9 6.2 6 Q9GWA3 159 7.6 608 11 Q9ZIAO 155 7.4 626 13 Q9WGJ7 153.5 7.3 918 13 Q9WGJ9 155 7.4 626 13 Q9WGJ9 155 7.3 918 13 Q9WGJ9 155 7.3 918 13 Q9WGJ9 155 7.2 206 4 Q8TD78 151 7.2 206 4 Q9GPJ5 Q9GP			13	538		•	39
222 10.6 368 6 Q8SQ71 Q8Sq71 s 212.5 10.1 278 11 Q9WHR8 Q8VHR8 Q8VhR8 1879 611 13 Q9HF6 Q9pTiO 185.5 8.8 343 13 Q9DEO1 Q9deq1 178.8 8.9 611 13 Q9HEO1 Q9deq1 175.5 8.3 896 11 Q9DEO1 Q9gth9 174.5 8.3 611 13 Q9PTH9 Q9pth9 173.5 8.3 891 13 Q9PTH9 Q9pth9 173.5 8.2 801 13 Q9PTH9 Q9pth9 175.5 8.2 801 13 Q9PTH9 Q9pth9 175.5 8.3 611 13 Q9PTH9 Q9pth9 Q9pth9 175.5 8.3 611 13 Q9PTH9	homo	Q96P35	4	376		ū	38
222 10.6 368 6 Q8SQ71 Q8Sq71 s 212.5 10.1 278 11 Q9LRF8 Q9whr8 187 8.9 611 13 Q9LRF6 Q9whr9 185.5 8.8 343 13 Q9DEQ1 Q9DEQ1 Q9deq1 174.5 8.3 896 11 Q8QZX9 Q8qZX9 Q9pth9 173.5 8.3 896 11 Q9PTH9 Q9ZX9 Q9pth9 173.5 8.3 811 13 Q9PTH9 Q9ZX9 Q9pth9 170 8.1 890 11 Q9ZLAO Q9pth9 170 8.1 890 11 Q9ZLAO Q9DJT Q9ZJAO Q9	homo	Q9UHJ5	4	349		151	37
222 10.6 368 6 Q8SQ71 Q8Sq71 s 212.5 10.1 278 11 Q9LBP6 Q9ibf6 11 13 Q9LBP6 Q9ibf6 Q9ibf6 11 13 Q9LBP6 Q9ibf6 Q9ibf6 11 13 Q9LBP6 Q9ibf6 Q9ibf6 11 Q9LBQ1 Q9BQ1 Q9BQ1 Q9BQ1 Q9BQ1 Q9BQ1 Q9BQ1 Q9BQ2 Q9	homo	Q96P36	4	288		151	36
222 10.6 368 6 Q8SQ71 Q8Sq71 s 212.5 10.1 278 11 Q8VHR8 Q8VHR8 Q8VhR8 187	homo		4	268		151	35
222 10.6 368 6 Q8SQ71 Q8Sq71 s 212.5 10.1 278 11 Q9UHR8 Q8VHR8 Q8Vhr8 187 8.9 611 13 Q9LBF6 Q9th6 187 8.9 611 13 Q9LBF6 Q9th1 185.5 8.8 343 13 Q9DEQ1 Q9deq1 175.5 8.3 896 11 Q6QZX9 Q8QZX9 174.5 8.3 896 11 Q6QZX9 Q9PTH9 173.5 8.3 896 11 Q9PTH9 Q9ZX9 Q9PTH9 173.5 8.3 811 13 Q9PTH9 Q9ZX9 Q9PTH9 175.5 8.3 811 13 Q9PTH9 Q9ZX9 Q9ZX9 176.7 9 622 6 Q9NOJ7 Q9ZX9 Q9ZX Q9ZX	homo		4	206	7.2	151	34
222 10.6 368 6 Q8SQ71 Q8Sq71 s 212.5 10.1 278 11 Q9LBP6 Q9ibf6 11 13 Q9LBP6 Q9ibf6 Q9ibf6 11 13 Q9LBP6 Q9ibf6 Q9ib		0	σ	217	7.3	153	ω
222 10.6 368 6 Q8SQ71 Q8Sq71 s 212.5 10.1 278 11 QVHR8 Q9 where 187 8.9 611 13 QVHR8 Q9 where 187 8.9 611 13 QVHR8 Q9 where 187 8.9 611 13 QVHR9 Q9 where 187 8.9 611 13 QVHY9 Q9 where 187 8.8 34 13 QVHY9 Q9 where 187 8.8 34 11 Q9 where 187 9.5 8.3 896 11 Q8CX9 Q9 where 187 9.5 8.3 896 11 Q9 where 187 9.5 8.3 896 11 QVHY9 Q9 where 187 9.5 8.3 891 13 QVHY9 QVHY9 Q9 where 187 9.5 8.3 891 13 QVHY9 Q9 where 187 9.5 8.3 891 13 QVHY9			13	918		153.5	32
222 10.6 368 6 Q8SQ71 Q8Sq71 s 212.5 10.1 278 11 Q9LBF6 187 8.9 611 13 Q9LBC0 185.5 8.8 343 13 Q9LBC0 195.5 8.8 896 11 Q6QLBC0 Q8qZx9 174.5 8.3 896 11 Q6QLBC0 Q8qZx9 174.5 8.3 896 11 Q9CX9 Q8qZx9 174.5 8.3 891 13 Q9CBPH Q9C	Q90wg7 cynop		13	626		155	31
222 10.6 368 6 Q8SQ71 Q8Sq71 s 212.5 10.1 278 11 Q9LHR8 Q9ibf6 187 8.9 611 13 Q9LHR8 Q9ibf6 187 8.9 611 13 Q9LHG Q9ibf6 185.5 8.8 343 13 Q9LHG Q9HG0 Q9ct10 178.5 8.8 896 11 Q6LHG Q9CX9 179.5 8.3 896 11 Q8QZX9 179.5 8.3 896 11 Q9CX9 Q9ct10 Q9ct10 179.5 8.3 896 11 Q9CX9 Q9ct10	Q9xs92 tricho	n	6	625	7.4	156	30
222 10.6 368 6 Q8SQ71 Q8Sq71 s 212.5 10.1 278 11 Q8VHR8 Q8VHR8 Q8VhR8 187 8.9 611 13 Q9FTO Q9ptiO 185.5 8.8 343 13 Q9FEO1 Q9deq1 175.5 8.3 896 11 Q8CX9 Q9ptiO 174.5 8.3 896 11 Q8CX9 Q9ptiO 173.5 8.2 881 13 Q9FH9 Q9pth9 173.5 8.2 881 13 Q9FH9 Q9pth9 173.5 8.2 881 13 Q9FH9 Q9pth9 167 7.9 622 6 Q9QLW3 Q9pth9 Q9pth9 167 7.8 227 6 Q9GLW3 Q9glw3 u Q9glw3 u	Q99jz1 mus n		11	808	•	159	29
222 10.6 368 6 Q8SQ71 Q8Sq71 s 212.5 10.1 278 11 Q8VHR8 Q8VhR8 Q8VhR8 187 8.9 611 13 Q9HP6 Q9pti0 185.5 8.8 343 13 Q9DEQ1 Q9deq1 175.5 8.3 896 11 Q8QXY9 Q8qXy9 174.5 8.3 611 13 Q9PTH9 Q9pth0 175.5 8.3 896 11 Q8QXY9 Q8qXy9 174.5 8.3 611 13 Q9PTH9 Q9pth0 173.5 8.3 896 11 Q8QXY9 Q8qXy Q9pth0 175.5 8.3 81 13 Q9PTH9 Q9pth0		n	σ	227	٠,	164	28
222 10.6 368 6 Q8SQ71 Q8Sq71 S 212.5 10.1 278 11 Q9HR8 Q9ibf6 187 8.9 611 13 Q9HF6 Q9ibf6 187 8.9 611 13 Q9HF0 Q9pti0 185.5 8.8 343 13 Q9DEQ1 Q9deq1 175.5 8.8 896 11 Q6H46 Q6H46 175.5 8.3 896 11 Q8QZX9 174.5 8.3 896 11 Q9PH9 Q9ZX9 173.5 8.2 881 13 Q9PH9 Q9ZX9 170 8.1 890 11 Q9ZX0 Q	C	Ω	σ	622		167	27
222 10.6 368 6 Q8SQ71 Q8Sq71 s 212.5 10.1 278 11 Q8VHR8 Q8VhR8 187 8.9 611 13 Q9FFF6 Q9th6 187 8.9 611 13 Q9FF10 Q9tt10 185.5 8.8 343 13 Q9DEQ1 Q9deq1 178 8.5 896 11 Q64146 Q64146 175.5 8.3 896 11 Q8QXX9 Q9EXP1 Q8QXP1 Q9DEQ1 174.5 8.3 611 13 Q9FH9 Q9Pth9 173.5 8.2 881 13 Q57519 Q57519			11	890		170	26
222 10.6 368 6 Q8SQ71 Q8Sq71 s 212.5 10.1 278 11 Q8VHR8 Q8Vhr8 187 8.9 611 13 Q9FF10 Q9pt10 185.5 8.8 343 13 Q9DEQ1 Q9deq1 175.5 8.3 896 11 Q8QXY9 Q9pth9 174.5 8.3 611 13 Q9FH9 Q9pth9 Q9pth9			13	881		173.5	25
222 10.6 368 6 Q8SQ71 Q8Sq71 s 212.5 10.1 278 11 Q8VHR8 Q8Vhr8 187 8.9 611 13 Q9TFG Q9pt10 185.5 8.8 343 13 Q9DFQ1 Q9deq1 175.5 8.3 896 11 Q8QZX9 Q8QZX9	xeno		13	611		٠	24
222 10.6 368 6 Q8SQ71 Q8Sq71 s 212.5 10.1 278 11 Q8VHR8 Q8Vhr8 187 8.9 611 13 Q9JBF6 Q9tt10 185.5 8.8 343 13 Q9DEQ1 Q9deq1 178 8.5 896 11 Q64146 Q64146	mus		11	896		•	23
222 10.6 368 6 Q8SQ71 Q8sq71 s 212.5 10.1 278 11 Q8VHR8 Q8vhr8 187 8.9 611 13 Q9FF10 Q9pti0 187 8.9 611 13 Q9FF10 Q9pti0 185.5 8.8 343 13 Q9DEQ1 Q9deq1			11	896	٠	178	22
222 10.6 368 6 Q8SQ71 Q8Sq71 s 212.5 10.1 278 11 Q8VHR8 Q8VhF8 187 8.9 611 13 Q9THF6 Q9btf6 187 8.9 611 13 Q9THT0 Q9pt10			13	343		185.5	21
222 10.6 368 6 Q8SQ71 Q8sq71 s 212.5 10.1 278 11 Q8VHR8 Q8vhr8 187 8.9 611 13 Q9IBF6 Q9ibf6			13	611		187	20
222 10.6 368 6 Q8SQ71 Q8sq71 s 212.5 10.1 278 11 Q8VHR8 Q8vhr8			13	611		187	19
222 10.6 368 6 Q8SQ71 Q8sq71 sus	8		11	278	,-	212.5	18
	sus		6	368		$\sim$	17

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Best Local
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01-DEC-2001
01-DEC-2001
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                         Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002996; CR1A.
InterPro; IPR003532; Hemtopoptn_S_F2.
PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Molecular cloning of canine IL-13 receptor alpha chain (alphal and alpha2) cDNAs and detection of corresponding mRNAs in canine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE=21287533; PubMed=11389954;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; (
Mammalia; Eutheria; Carnivora; 
MCBI_TaxID=9615;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Canis familiaris (Dog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q95LF0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Vet. Immunol. Immunopathol. 79:181-195(2001). EMBL; AF314533; AAL14887.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tissues.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ol-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2002 (TrEMBLrel. 20, Last annotation update)
Interleukin 13 receptor alpha chain 2.
1 MAFVCLAIGCLYTFLISTTFGCTSSSDTEIKVNPPQDFEIVDPGYLGYLYLQWQPPLSLD
                                                                                                                                                MAFIHLDVGFLYTLLVCTAFG-SMLSNAEIKVNPPQDFEIVDPGYLGYLSLQWQPPLFPD
                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                         386 AA;
                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                     45110 MW; A16FDF2DD023ED95 CRC64;
                                                                                                                                                                                                                                                                                                                      71.4%;
72.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chordata; Craniata; Vertebrata; Euteleostomi; Carnivora; Fissipedia; Canidae; Canis.
                                                                                                                                                                                                                                                                                                42;
                                                                                                                                                                                                                                                                                        Score 1503; DB 6;
Pred. No. 1.2e-121;
2; Mismatches 57;
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                                                                                                                                                                                                            Query Match
Best Local S
Matches 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.

STRAIN-C3H/HEJ; TISSUE-THYMUS;
MEDLINE-98391042: PubMed-9725226:
Donaldson D.D., Whitters M.J., Fitz L., Neben T.)
Henderson S.L., O'Hara R.M. Jr., Beier D.R., Turn
Collins M.;
"The murine IL-13 receptor alpha 2: molecular clc
characterization, and comparison with murine IL-
J. Immunol. 161:2317-2324(1998).
                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.;
Submitted (FEB-2001) to the EMF
Submitted (FEB-2001) to the EMF
EMBL; U65747; AAC33240.1; -.
EMBL; BC003723; AAH03723.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  088786;
01-NOV-1998
01-NOV-1998
01-MAR-2002
                                                                                                                                                                                                                                                                                                                     InterPro; IPR002996; CR1A.
InterPro; IPR003532; Hemtopoptn_S_F2.
PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; C
Mammalia; Eutheria; R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                        Receptor.
                                                                                                                                                                                                                                                                                                                                                                                HSSP; P16471; 1BP3.
MGD; MGI:1277954; Ill3ra2.
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                       121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           359
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                                                                                                                                ALQCVDYIKADGQNIGCRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLP::||||||:||:|||||||:||:||
saectdyikvngknmgcrfpylessdykdfyicvngssesqpirpsyfifqlqnivkpmp
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                                                        HFKECTVEYELKYRNIGSETWKTIITKNLHYKDGFDLNKGIEAKIHTLLPWQCTNGSEVQ 120
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                                                                                                                                                                                                              l Similarity
219; Conserv
                                                                                                                                                                                                                                                                                      383 AA;
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                                                                                                                                                                                                              Conservative
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Rodentia;
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                                                                                                                                                                                                                                                                                      44482 MW;
                                                                                                                                                                                                                              56.8%;
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Last sequence up
Last annotation
                                                                                                                                                                                                            Score 1194.5;
Pred. No. 5.3e
55; Mismatches
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                                                                                                                                                                                                                                                                                      C25212325C47E35B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       molecular cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              383
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                                                                                                                                                                                                            5; DB 11; Length
.3e-95;
es 91; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      update)
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Turner
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Best Local S
Matches 211
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Q8VHK6;
01-MAR-2002
01-MAR-2002
01-JUN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Molecular cloning of rat interexpression in rat tissues."; submitted (NOV-2001) to the EMEMBL; AF448818; AAL57513.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002996; CR1A.
InterPro; IPR003532; Hemtopoptn_S_F2
PROSITE; PS01356; HEMATOPO_REC_S_F2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10116
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                         SSWAETTYWISPQGIPETKVQDMDCVYYNWQYLLCSWKPGIGVLLDTNYNLFYWYEGLDH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TRQLCFVVRSKVNIYCSDDGIWSEWSDKQCWEGEDLSKKTLLRFWLPFGFILILVIFVTG
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                                                                                                                        PVYLTFTRESSCEIKLKWSIPLGPIPARCEDYEIEIREDDTTLVTATVENETYTLKTTNE
                                                                                                                                                                                             ALQCVDYIKADGQNIGCRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLP
                                                                                                                                                                                                                                                                                               SPWTEASYGIADEGSLGTKIQDMKCIYYNWQYLVCSWKPGKTVHSDTNYTMFFWYEGLDH
                                                                                                                                                                                                                                                                                                                                                                                              NFKECKLEYELKYRNVDSDSWKTIITRNLIYKDGFDLNKGIEGKIRTHLSEHCTNGSEVQ
                                                                                                                                                                                                                                                                                                                                                                                                                       HFKECTVEYELKYRNIGSETWKTIITKNLHYKDGFDLNKGIEAKIHTLLPWQCTNGSEVQ 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MALMAVNTRCLCLFLLCTITG----HSLEIKVNPPQDFEILDPGLLGYLYLQWKPPVVMD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEDLCFFVRCKVNIYCADDGIWSEWSEEECWEGYTGPDSKII-FIVPVCLFFIFLLLLLC
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11; Conservative
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(TrEMBLrel. 20, Last sequence update)
(TrEMBLrel. 21, Last annotation updat
13 receptor alpha chain 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA;
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Rodentia;
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56.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EE06FF0E434737E2 CRC64;
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; Murinae; Rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N
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Q14633;
Q1-NOV-1996
Q1-NOV-1996
Q1-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Isolation and characterization of a putative interleukin alpha-2 sequence from rainbow trout (Oncorhynchus mykiss). Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF361437; AAL26927.1; InterPro; IPR002996; CRIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleost
Actinopterygii; Meopterygii; Teleostei; Buteleostei;

Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

NCBI_TaxID=8022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              090xP8;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation updat
Interleukin 13 receptor alpha-2.
              Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                  01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation updat
Interleukin-5 receptor precursor.
                                          Homo sapiens
                                                       HSIL5R.
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                                                                                                                                                                                                                         RSKVNIYCSDDGIWSEWSDKQCWEGEDLSKKTLLRFWLPFGFILILVIFVTGLLL
                                                                                                                                                                                                                                                                           EIKLKWSIPLGPIPARCEDYEIEIREDDT---TLVTATVENE-TYTLKTTNETRQLCFVV
                                                                                                                                                                                                                                                                                                                                 IGCRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNIVKP--LPPVYLTFTRESSC
                                                                                                                                                                                                                                                                                                                                                                     PVGSRVQGFGCVFYQKEFMECTWETGLEEPTQSQYSLYFWHREMEQAEECPQYIHSNGVR
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                                                                                                                                                                                                         RSRMHHYCADRGFWSDWSHWSC--HSDTESDAVV-----
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               3 (Human).
3 (Human).
Chordata;
1 mates;
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                                                                                                                                      PRELIMINARY;
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Pred. No. 7.6e
74; Mismatches
               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                      PRT;
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6e-42;
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RESULT
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                                                                                                                                                                  01-NOV-1996
01-NOV-1996
01-MAR-2002
                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
SEQUENCE
       J. Exp. Med. :
EMBL; X61177;
                                    TISSUE-PERIPHERAL BLOOD;
MEDLINE-92121815; PubMed=1732409;
MUTATA Y. Takaki S., Migita M., I
"Molecular cloning and expression
                                                                                                                                                                                                            Q14631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-PERIPHERAL BLOOD;
MEDLINE-92121815; PubMed-1732409;
Murata Y., Takaki S., Migita M.,
                                                                                                                                                                                                  Q14631;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002996; CR1A.
InterPro; IPR003532; Hemtopoptn_S_F2.
PROSTTE; PS01356; HEMATOPO_REC_S_F2;
                                                                                                   NCBI_TaxID=9606;
                                                                                                                                               HSIL5R2.
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                            receptor
                                                                                SEQUENCE FROM N.A.
                                                                                                                                                       01-MAR-2002 (TrEMBLrel.
Interleukin-5 receptor
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Local Similarity
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                                                                                                                                                                                                                                                                                                       RAAVSSMCREAGLWSEWS-QPIYVGNDEHKP--LREW----FVIVIMATICFILLILSLI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100;
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      175:341-351(1992).
; CAA43484.1; -.
                                                                                                                                                                                                            PRELIMINARY;
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420 I
47670 MW;
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Pred. No. 9.9e
69; Mismatches
                                                                                                                                                     Last sequence update)
Last annotation update
2 precursor.
                                                                                                                                                                                     Created)
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; 8DC56DFC8BEFF524 CRC64;
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hes 156;
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                                     Y., Tominaga A., human interleukin
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                                       Takatsu
n 5
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RESULT 7
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Best Local S
Matches 99
            Query Match
                                              Receptor.
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Eukaryota; Metazoa; Ch
Mammalia; Eutheria; Ca
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SIGNAL
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01-DEC-2001 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
Interleukin 13 receptor
                                                                                                                  Vet. Immunol. Immunopathol. 79:181-195(2001). EMBL; AF314532; AAL14886.1; -. Interpro; IPR002996; CR1A.
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PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
                                   SEQUENCE
                                                                    PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1
                                                                                   InterPro; IPR003532; Hemtopoptn_S_F2
SMART; SM00060; FN3; 1.
                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=21287533; PubMed=11389954;
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                                                                                                                                                                      alpha2) cDNAs and
                                                                                                                                                                                                                                          NCBI_TaxID=9615;
                                                                                                         InterPro;
                                                                                                                                                                                 'Molecular cloning
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Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  LRKPNTYPKMIP 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RAAVSSMCREAGLWSEWS-QPIYVGNDEHKP--LREW----FVIVIMATICFILLILSLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RSKVNIYCSDDGIWSEWSDKQCWEGEDLSKKTLLRFWLPFGFILIL-----VIFVTGLL
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                                                                                                         IPR003961; FN_III.
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396 /
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                                                                                                                                                                     detection
                                                                                                                                                                  of canine IL-13 receptor alpha detection of corresponding mRNAs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20
396
44998
                                                                                                                                                                                                                                                      Chordata; Craniata; Vertebrata; Carnivora; Fissipedia; Canidae;
                                   46328 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.8%;
26.6%;
14.48; 27.28;

    Created)
    Last sequence update)
    Last annotation update)
    Alpha chain 1 (Fragment).

                                                                                                                                                                                                                                                                                                      alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 310.5;
Pred. No. 1.1e
70; Mismatches
Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INTERLEUKIN-5 RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1AB60619842ACDA5 CRC64;
                                   926E1AC7BE5E3F42 CRC64;
302.5; DB 6;
No. 5.7e-18;
                                                                                                                                                                                                                                                                                                                                                                 405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1.1e-18;
hes 156;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4;
                                                                                                                                                                     mRNAS
                                                                                                                                                                   chain (alphal
s in canine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                      Euteleostomi;
Canis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE
           405;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           396;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47;
                                                                                                                                                                                and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          361
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                                                                                                                                                          Query Match
Best Local
                                                                                                                                               Matches 103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9Z0K4;
Q9Z0K4;
Q1-MAY-1999
01-MAY-1999
01-JUN-2002
                                                                                                                                                                                                                           SIGNAL
                                                                                                                                                                                                                                                 Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases EMBL; U55215; AAD09361.1; -.
InterPro; IPR002996; CR1A.
InterPro; IPR003532; Hemtopoptn_S_F2.
PROSITE; P901356; HEMATOPO_REC_S_F2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                  Cavia porcellus (Guinea pig).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                      "Cloning and Characterization of the Guinea Pig Interleukin-5 receptor alpha cDNA.";
                                                                                                                                                                                                                                                                                                                                                                                                                                          GPIL-5RA.
                                                                                                                                                                                                                CHAIN
                                                                                                                                                                                                                                                                                                                                                  Norris T.E.
                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                        Receptor; Signal.
                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=10141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interleukin-5 receptor alpha
             126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   193
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                                         59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      53
                                                                                                                                                            Local Similarity
                                                                                                                     6
                                                                                                                  LAIGCLYTFLISTTFGCTSSSDTEIKVNPPQDFEIVDPGYLGYLYLQWQPPLSLDHFKEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MIPEFFCD 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TNYNLEYWYEGLDHALQCVDYIKADGQNIGCRFPY--LEASDYKDFYICVNGSSENKPIR
             TTYWISPQGIPETKVQDMDCV-----YINWQ----YILCSWKPGIGVLLDTNYNLFY-
                                        NLNYHVKINTPQEEDYE---TRNTQSKCETTLHQGVSASVRTIL-WH--GHSLLASSWVS
                                                                TVEYELKYRNIGSETWKTIITKNLHYKDGFDLNKGIEAKIHTLLPWQCTNGSEVQSSWAE
                                                                                           ILLGAIETLQTDTL-----PDKKFLLLPPINFTIKVTG-LAQVVLCWEPNPNQGQ-KNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IFKEMFGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NWS-----QAMSIGENTDPTFYITMLLATQVIVAGAIIILLLYLKRLKIIIFPPIPDPGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SSYFTFQLQNIVKPLPP-VYLTFTRESSCEIKLKWSIPLGPIPARCFDYEIEIREDDTT-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LLPWQC-TNGSEVQSSWAETTYWISPQGIPETKVQDMDCVYYNWQYLLCSWKPGIGVLLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EWSDKQCWEGEDLSKKTLLRFWLPF-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NDIFYVEEAKCQNSEF---EGNLEGTICFMVPGVLPDTLNTVRIRVRTNKLCYEDDKLWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PSFNIVPLTSHVKPDPPHIKRLFFQNGN--LYVQWKNPQN-FYSRCLSYQVEVNNSQTET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TNYTLYYWHSSLGKILQCED-IYREGQHIGCSFALTNLKDSSFEQHSVQIMVKDNARKIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----QCSTNESDNPSILVEKC-TPPPEGDPESAVTELQCVWHNLSYMKCTWLPGRNTSPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WNPPEGAS--PNCTLRYFSHFDNKQDKKIAPET-----HRSKEVPLNERICLQVGS 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WQPPLSLDHFKECTVEYELKYRN-----IGSETWKTIITKNLHYKDGFDLNKGIEAKIHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100;
---:
                                                                                                                                                                                                  415 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrembLrel. 10, Created)
(TrembLrel. 10, Last seq
(TrembLrel. 21, Last ann
                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          369
                                                                                                                                                                                                                415
                                                                                                                                                                                                  46913 MW;
                                                                                                                                                                                                                               17
                                                                                                                                                            14.2%;
26.5%;
                                                                                                                                            67;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
Last annotation update)
                                                                                                                                                         Score 298.5; DB 1
Pred. No. 1.3e-17
                                                                                                                                                                                                               POTENTIAL.
INTERLEUKIN-5 RECEPTOR ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                       precursor
                                                                                                                                                                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi;
Hystricognathi; Caviidae; Cavia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                  41BA4BA597B31CD4 CRC64;
                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -GFILILVIFVTGL--LLRKPNTYP-K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Å
                                                                                                                                                                        DB 11;
_
<u>:</u>
                                                                                                                                              172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142;
                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                       Length 415;
                                                                                                                                               47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                69;
                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       192
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                                                                                           58
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                                                                                                                                               19;
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Qy
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                                                                                                                                                                                                                                                                                                                        SO
                                                                                                                                                                                                                                                                 Query Match
Best Local S
Matches 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OLT
BB4
                                                                                                                                                                                                                                                                                                                        Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          096BB4: Q8WX08;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Interleukin 13 receptor, alpha 1 (BB12804.2.1).
                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JAN-2002) to the EMBL/GenBank/DDBJ EMBL; BC015768; AAH15768.1; -. EMBL; AL391280; CAD21446.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q96BB4
                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002996; CR1A.
InterPro; IPR003961; FN_III.
InterPro; IPR003332; Hemtopoptn_S_F2
SMART; SM00060; FN3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=COLON;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                               PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lawlor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 31-427 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
               235
                                                                                                                           118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       340
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                                                                                                108
                                                                                                                                                      61
                                                                                                                                                                                  64
                                                                                                                                                                                                            ω
                                                                                                                                                                                                                                       σ
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IVKPLPP--VYLTFTRESSCEIKLKWSIPLGPIPARCFDYEIEIREDDTT-----LVTA
                                                                                                              EVQSSWAETTYWIS-PQGIPETKVQDMDCVYYNWQYLLCSWKPGIGVLLDTNYNLFYWYE
                                                                                                                                                   NCSLWYFSHFGDKQDKKIAPETRRSI-----EVPLNERICLQVGS----QCSTNES
                                                                                                                                                                                                          CPARLCGLWALLLCAGGGGGGGGAAPTETQPPVTNLSVSVENLCTVIWTWNPPEGAS--S
                                                                                                                                                                                                                                   CLAIGC-LYTFLISTTFGCTSSSDTEIKVNPPQDFEIVDPGYLGYLYLQWQPPLSLDHFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FTFQLQNIVKPLPPVYLTFTRESSCEIKLKWSIPLGPIPARCFDYEIEI-REDDTTLYTA
                                        SLEKIHQC-ENIFREGQYFGCSFDLTKVKDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTS
                                                                  GLDHALQCVDYIKADGQNIGCRFPYLEASD--YKDFYICVNGSSENKPIRSSYFTFQLQN
                                                                                               EKPSILVEKC--ISPPEGDPESAVTELQCIWHNLSYMKCSWLPGRNTSPDTNYTLYYWHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      :: : : : : | | : : | | |
ITLTAVLCFILLIFFFLCRIYHLWTKMFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LPFGFILILVIFVTGLLLRKPNTYPKMIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTTNA--FVSTTDGVSKYSIQVRAAVSPHCRAMGLWSKWS-QPVYVGKE--KKPIAGWFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QLFDTQAIDQPNPPMDVTAETEGS-RLSIQWQKPVSAFPIHCFEYEVKICNTKDYYQVEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YGPWTE-----ECQEYSKDTLSRNTACWFPRTFIHSKARDRLAVHVNGSSNHATIKPFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AEH-KAPPGSPGTSIVNLTCTTNTAASNYTNLKSYEVSLHCTWLAGKDAPEDTQYFLYYR
                                                                                                                                                                                                                                                                   al Similarity
110; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -WYEGLDHALQCVDYIKAD-GQNIGCRFP--YLEASDYKDFYICVNGSSENKPIRSSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (OCT-2001) to
                                                                                                                                                                                                                                                                                                                        427
                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                        A
                                                                                                                                                                               ELKYRNIGSETWKTIITKNLHYKDGFDLNKGIEAKIHTLLPWQC-TNGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chordata;
Primates;
                                                                                                                                                                                                                                                                                                                        48676 MW;
                                                                                                                                                                                                                                                              14.1%; Score 297; DB 4; Length 427; 26.3%; Pred. No. 1.8e-17; Live 63; Mismatches 172; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                       E6A42F7466A39A09 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       368
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Best Local S
Matches 97
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01-MAR-2002 (TrEMBLrel 2)
01-JUN-2002 (TrEMBLrel 2)
IL-13 receptor alpha 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
STRAIN-FISHER F344;
MEDLINE-21458304; PubMed=11573960;
MEDLINE-21458304; PubMed=11573960;
Pierrot C., Beniquel L., Begue A., Khalife J.;
"Expression of a functional IL-13Ralphal by rat B cells.";
Biochem. Biophys. Res. Commun. 287:969-976(2001).
EMBL; AY044251; AAK94870.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q8VHC2
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InterPro; IPR003532; Hemtopoptn_S_F2.
PR0SITE; PS01356; HEMATOPO_REC_S_F2;
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                                                                                                                                                                                                                                                                                              MDCVYYNWQYLLCSWKPGIGVLLDTNYNLFYWYEGLDHALQCVDYIKADGQNIGCRFPYL
                                                                  LIIPVFVAVVII
                                                                                           LILVIFVTGLLL
                                                                                                                      VYTVRVRVKTNKLCF---
                                                                                                                                              TYTLKTTNETRQLCFVVRSKVNIYCSDDGIWSEWSDKQCWEGEDLSKKTLLRFWLPFGFI
                                                                                                                                                                                          PLGPIPARCFDYEIEIREDDTT------
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                                                                                                                                                                                                                                                                                                                                                                                      EVQPPVTNLSVSVENLCTIVWTWSPPEGAS--PNCSLRYFSHFDDQQDKKIAPETRR---
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                                                                                                                                                                        PQN-FSSRCLSYEVEVNSTQTDSYNSNSLEVEEDKCQNSEFDRNMEGASCFISPGVLANT
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97; Conser
                                                                                                                                                                                                                                                                                                                                   KKELPLNEKICLQVGS----QCSTNESEKPSPLVKKC--ISPPRRG-SESAVTE
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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Last annotation update)
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Pred. No. 2.2e-17;
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                                                                                                                     -DDNDLWSNWS-----EALSIGKEPNSTFYTT--ML
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Q15469

PRELIMINARY;

PRT;

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the 5'-upstream region

and

expression

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RESULT
Q920B
ID
Q0
DT
Q0
DT
Q1
                                                                                                                O920B8

O920B8;

O920B8;

O1-DEC-2001 (TrEMBLrel. 19, Created)

O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)

OT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)

DE Interleukin-5 receptor alpha.

OR Rattus norvegicus (Rat).

Marazoa; Chordata; Craniata; Vertebrata;

Marazoa; Chordata; Sciurognathi; Murida;
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O1-NOV-1996 (TrEMBLrel. C
O1-NOV-1996 (TrEMBLrel. C
O1-MAR-2002 (TrEMBLrel. 2
Soluble interleukin-5 re
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TISSUE-PERIPHERAL BLOOD;
MEDLINE-92121815; Pubmed-1732409;
Murata Y., Takaki S., Migita M., Kikuchi
"Molecular cloning and expression of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SIGNAL
  "Molecular cloning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002996; CRIA.
InterPro; IPR003532; Hemtopoptn_S_F2.
PROSITE; PS01356; HEMATOPO_REC_S_F2;
                                             STRAIN-F344;
                                                                    SEQUENCE FROM N.A.
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EMBL; X62156; CAA44081.1; -.
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Mammalia; Eutheria;
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Homo sapiens (Human).
Chordata;
                                                                                                              NCBI_TaxID=10116;
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333 AA;
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28.0%;
  Szpirer C., Capron characterization
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01, Last sequence update)
20, Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOLUBLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POTENTIAL
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  of rat IL-5Ra
                                                                                                                                                       Vertebrata; Euteleostomi;
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                                                                                                                                     Muridae;
                                                                                                                                                                                                                          update)
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gene
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Best Local :
                                          NON_TER
NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last Sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Interleukin-13 receptor alpha-1 chain (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (NOV-2000) to the EMBL/GenBank/DDBJ dEMBL; AF324153; AAK97344.1; -.
InterPro: IPR002996; CRIA.
InterPro: IPR003532; Hemtopoptn_S_F2.
PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
                                                                                                                                                                                                                                bovine cells.";
Vet. Immunol. Immunopathol.
                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=20080132; Pubmed=10614495;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                          PROSITE;
                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                Trigona W.L., Brown W.C., Est
"Functional implications for
                                                                                                                                                                                                                                                                                                                                                                                                                     Bovidae; Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bos taurus (Bovine)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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                                                                                                                  Receptor.
                                                                                                                                                               InterPro;
                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9913;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RFW----LPEGFILILVIFVTGLLLRKPNTYPKMIP 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STTFGCTSSSDTEIKVNPPQDFEIVDPGYLGYLYLQWQP-----PLSLDHFKECTVEYEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AIDQVNPPMNVTVEIENN-SLYIQWGKPLSAFPVHCFKYKLKIYNTKNGYSQMENLVTNK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NIVKPLPPVYLTFTRESSCEIKLKWSIPLGPIPARCEDYEIEIREDDT-----TLVT--
                                                                                                                                                                                                               AF074402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FISKIDDVSTYSIQ-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             --ATVEN-ETYTLKTTNETRQLCFVVRSKVNIYCSDDGIWSEWSDKQCWEGEDLSKKTLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----ECQEYSRDALNRNIACWFPRTFINSKGFEQLAVHINGSSKHAAIKPLDQLFTLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GLDHALQCVDYIK-ADGQNIGCRFP--YLEASDYKDFYICVNGSSENKPIRSSYFTFQLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPGSSGTSVMNLTCTTNTVKSSHTHFRPYQVSLRCTWLVGKDAPEDTQYFLYYRFSVWTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PQGIPETKVQDMDCV-----YYNWQY-LLCSWKPGIGVLLDTNYNLFY----WYE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KYRNIGSETWKTIITKNLHYKDGFDLNKGIEAKIHTLLPWQCTNGSEVQSSWAETTYWIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             103;
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                                                                                                                                          PS01356;
                                                                                                                            IPR002996; CR1A.
IPR003532; Hemtopoptn_S_F2.
PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1
                                               349
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                                                                     1
349
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                                               Ā
                                                                                                                                                                                                             AAC98147.1;
                                                                                                                                                                                                                                                                                                                                                                                                                        Bos.
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                                             39644 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12.7%;
  12.6%;
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                                                                                                                                                                                                                                  72:73-79(1999)
                                                                                                                                                                                                                                                                                signaling
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4; Mismatches
  Score
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                                               D61A4C918B1940A6 CRC64;
                                                                                                                                                                                                                                                                                                     D.M.;
  264.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              349
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  Length 349;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Bovoidea;
                                                                                                                                                                                                                                                                                complex
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Best Local Matches

83; Conservative (

63; Mismatches 1

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RESULT COPERS OF                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    δÃ
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                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q99PS3;
Q1-JUN-2001 (TrEMBLrel. 17, Created)
Q1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
Q1-JUN-2001 (TrEMBLrel. 20, Last annotation update)
Q1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Interleukin-5 receptor alpha chain precursor.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalla; Eutherla; Rodentia; Sciurognathi; Muridae
MCBI_TaxID-10116;
                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  subunit.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ
EMBL; AB056101; BAB32866.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR003532; Hemtopoptn_S_F2.
SMART; SM00060; FN3; 2.
PROSITE; PS01336; HEMATOPO_REC_S_F2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN-SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q99PS3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR002996; CR1A.
InterPro; IPR003961; FN_III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ishihara K., Asai K., Ohuchi K.;
"Identification of cDNA encoding
  116
                                                    132
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PPGSSGTSVMNLTCTTNTVKSSHTHFRPYQVSLRCTWLVGKDAPEDTQYFLYYRFSVWTE
                                PQGIPETKVQDMDCV------YYNWQY-LLCSWKPGIGVLLDTNYNLFY----WYE
                                                                                                                                                                                                        SATLHADLLSPEKFLLLPPVNFTIKATG-LAQVLLHWDPNPDQDPVDLEYHVKINVPQED
                                                                                                                                                                                                                                      STTFGCTSSSDTEIKVNPPQDFEIVDPGYLGYLYLQWQP-----PLSLDHFKECTVEYEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FYWYEGLDHALQCVDYIKADGQNIGCRFPYLEASD--YKDFYICVNGSSENKPIRSSYFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NETYTLKTTNETR------QLCFVV------RSKVNIYC-SDDGIWS
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                                                                                                                                                                                                                                                                                                                   101;
                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                         414 AA;
                                                                                                                                                                                                                                                                                                              12.3%; Score 259; DB 11; larity 25.5%; Pred. No. 3.3e-14; Conservative 65; Mismatches 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -QAMSIGQKANQTEYIT--TLLIIPVIVAAAVI
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                                                                                                  -TKNTESKCVTPLHECFAASVRTILK---SIHSPLASSWVSAEL-KA
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POTENTIAL.
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Sciurognathi; Muridae;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                Receptor.
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. Wada M.; Hisano T., Kuwano M.; Submitted (JUN-1999) to the EMEMBL; U81380; AAD00511.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequ
01-MAR-2002 (TrEMBLrel. 20, Last anno
Interleukin-13 receptor soluble form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9UDY5;
                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002996; CR1A.
InterPro; IPR003532; Hemtopoptn_S_F2.
PROSITE; PS01356; HEMATOPO_REC_S_F2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                       LWALLLCAGGGGGGGAAPTETQPPVTNLSVSVENLCTVIWTWNPPEGAS--SNCSLWYF
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                                                                                                           CVDYIKADGQNIGCRFPYLEASD--YKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RFW----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --ATVEN-ETYTLKTTNETRQLCFVVRSKVNIYCSDDGIWSEWSDKQCWEGEDLSKKTLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AIDQVNPPMNVTVEIENN-SLYIQWGKPLSAFPVHCFKYKLKIYNTKNGYSQMENLVTNK
                                     HIKNLSFHND----DLYVQWENPQNFI-SRCLFYEVEVNNSQT
                                                                                          C-ENIFREGQYFGCSFDLTKVKDSSFEQHSVQIMVKDNAGKIKPSFNIVPLTSRVKPDPP
                                                                                                                                              EKC -- ISPPEGDPESAVTELQCIWHNLSYMKCSWLPGRNTSPDTNYTLYYWHRSLEKIHQ
                                                                                                                                                             ETTYWIS-PQGIPETKVQDMDCVYYNWQYLLCSWKPGIGVLLDTNYNLFYWYEGLDHALQ
                                                                                                                                                                                                   SHEGDKQDKKIAPETRRSI-----EVPLNERICLQVGS----QCSTNESEKPSILV
                                                                                                                                                                                                                    ----ELKYRNIGSETWKTIITKNLHYKDGFDLNKGIEAKIHTLLPWQC-TNGSEVQSSWA 124
                                                                --VYLTFTRESSCEIKLKWSIPLGPIPARCFDYEIEIREDDT
                                                                                                                                                                                                                                                                                                           . Similarity 78; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -ECQEYSRDALNRNIACWFPRTFINSKGFEQLAVHINGSSKHAATKPLDQLFTLY
                                                                                                                                                                                                                                                                                                                                                                279 AA;
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                                                                                                                                                                                                                                                                                                            Conservative
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27.7%;
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Last annotation update)
                                                                                                                                                                                                                                                                                                           Score 241.5; DB 4;
Pred. No. 6.7e-13;
5; Mismatches 126;
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19:36:18
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Minimum
Maximum
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Maximum Match 10
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## ALIGNMENTS

RESULT S21052

#### A:Molecule type: mRNA A;Residues: 1-128,'I','130-332,'K' <MU4> A;Residues: 1-128,'I','130-332,'K' <MU4> A;Cross-references: EMBL:X62156; NID:g36465; PIDN:CAA44081.1; PID:g36466 A;Cross-references: EMBL:X62156; VID:g36465; PIDN:CAA44081.1; PID:g36466 C;Keywords: alternative splicing; cytokine receptor; glycoprotein; transmemb: F;1-20/Domain: signal sequence #status predicted <SIG> F;21-420/Product: interleukin-5 receptor alpha chain #status predicted <MAT> C;Species: Homo sapiens (man) C;Date: 22-Nov-1993 #sequence\_revision 10-Nov-1995 #text\_change 01-Dec-2000 C;Accession: S21052; S21050; S21053; A46175; S78106; S78107 C;Accession: S21052; S21050; S21053; A46175; S78106; S78107 C;Accession: S21052; S21050; S21053; A46175; S78106; S78107 C;Accession: S21052; S21053; A46175; S78107 C;Accession: S21052; S21052; S21053; A46175; S78107 C;Accession: S21052; S21052; S21053; A46175; S78107 C;Accession: S21052; A46175; A46 A; Molecule type: DNA A; Residues: 1-395,'I' <MU2> A; Cross references: EMBL:X61177; NID:g33839; A; Experimental source: clone lambda h5R.27 A; Reference number: A; Accession: S78107 A; Molecule type: mR submitted to the EMBL Data A; Reference number: \$78107 A;Cross-references: EMBL:X61177; NID:g33839; PIDN:CAA43484.1; PID:g33840 A; Molecule type: DNA A; Residues: 1-128, 'I', 130-395, 'I' < MUW> A; Reference number: A; Accession: S78106 submitted to the EMBL Data A; Reference number: \$78106 A; Experimental source: HL-60 cells and eosinophils A; Note: sequence extracted from NCBI backbone (NCBIN:116243, NCBIP:116244) A; Molecule type: mRNA A; Residues: 333-420 <TAV> A;Title: Molecular basis of A;Reference number: A46175; A;Accession: A46175 A;Cross-references: EMBL:X62156; NID:g36465; PIDN:CAA44081.1; PID:g36466 A;Experimental source: clone lambda h5R.25 R;Tavernier, J.: Tuypens, T.; Plaetinck, G.; Verhee, A.; Fiers, W.; Devo: Proc. Natl. Acad. Sci. U.S.A. 89, 7041-7045, 1992 A; Molecule type: mRNA A; Residues: 1-332, 'K' <MU3> A; Cross-references: EMBL: X61176; NID: 933843; A; Experimental source: clone lambda h5R.12 A; Molecule type: A; Residues: 1-42 A; Title: Molecular cloning and expression of the human interleukin 5 receptor A; Reference number: S21050; MUID:92121815; PMID:1732409 R;Murata, R; Murata, A; Accession: S21053 A; Accession: S21050 A; Accession: S21052 interleukin-5 receptor alpha chain precursor (clone lambda h5R.12), membrane-anchored Status: preliminary 1-420 <MUR> DNA Library, September 1991 Library, July 1991 the membrane-anchored and two soluble isoforms MUID:92357767; PMID:1495999 PIDN:CAA43483.1; PIDN:CAA43484.1; PID:g33840 PID: 933844 W.; Devos, of the mud

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A;Title: Expression of a functional IL-JaRalphal by A;Reference number: JC7773; PMID:11573960
A;Accession: JC7773
A;Molecule type: mRNA
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A;Residues: 1-426 <PIE>
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   KVESNYEHHNIQIMVKDNAGKIRPSYKIVSFTSNVKPGPPHIKHLFLKNGA--LFVQWKN
                                       EA-SDYKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLPP-VYLTFTRESSCEIKLKWSI 260
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                                                                       LQCTWHNLSYMKCSWLPGKNTSPDTNYTLYYWYSSLGKSLQC-ENIHREGQHIGCSFKLT
                                                                                                       MDCVYYNWQYLLCSWKPGIGVLLDTNYNLFYWYEGLDHALQCVDYIKADGQNIGCRFPYL 202
                                                                                                                                           -----KKELPLNEKICLQVGS----QCSTNESEKPSPLVKKC--ISPPRRG-SESAVTE 129
                                                                                                                                                                           TKNLHYKDGFDLNKGIEAKIHTLLPWQC-TNGSEVQSSWAETTYWISP--QGIPETKVQD 142
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C; Accession: JQ1655
R; Tanaka, M.; Maeda, K.; Okubo, T.; Nakashima, K.
Biochem. Blophys. Res. Commun. 188, 490-496, 1992
A; Title: Double antenna structure of chicken prolactin receptor deduced A; Reference number: JQ1655; MUID:93075121; PMID:1445292
A; Accession: JQ1655
A; Molecule type: mRNA
A; Residues: 1-831 <TAN>
                                                                                                                                     prolactin receptor precursor - chicken
C; Species: Gallus gallus (chicken)
C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Title: A human high affinity interleukin-5 receptor (IL5R) A;Reference number: A40267; MUID:92005669; PMID:1833065 A;Accession: A40267 A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Tavernier, J.; Devos, R.; Cornelis, S.; Tuypens, T.; Van der Heyden, J.; Fiers, Cell 66, 1175-1184, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      interleukin-5 receptor alpha chain precursor - human
c;Species: Homo sapiens (man)
C;Date: 17-Jan-1992 #sequence_revision 17-Jan-1992 #text_change 05-Nov-1999
C;Accession: A40267
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A; Residues: 1-335 <TAV>
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                                                                                                                                         LGRNIACWFPRTFILSKGRDWLSVLVNGSSKHSAIRPFDQLFALHAIDQINPPLNVTAEI
                                                                                                                                                                                                                                                                                                                                                                                      DTEIKVNPPQDFEIVDPGYLGYLYLQWQPPLSLDHFKECTVEYELKYRNIGSETWKTIIT 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LIIPVFVAVVII 360
RAAVSSMCREAGLWSEWS
                                  RSKVNIYCSDDGIWSEWS
                                                                                                                                                                                                             THTTEDNYSRLRSYQVSLHCTWLVGTDAPEDTQYFLYYRYGSWTE-----ECQEYSKDT 189
                                                                                                                                                                                                                                                                                 ES---KCVTILHKGFSASVRTILQ---NDHSLLASSWASAELH-APPGSPGTSIVNLTCT 135
                                                                                                                                                                                                                                                                                                                  KNLHYKDGFDLNKGIEAKIHTLLPWQCTNGSEVQSSWAETTYWISPQGIPETKVQDMDCV 146
                                                                                                                                                                                                                                                                                                                                                       DEKISLLPPVNFTIKVTG-LAQVLLQWKPNPDQEQ-RNVNLEYQVKINAPKEDDYETRIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PQN-FSSRCLSYEVEVNSTQTDSYNSNSLEVEEDKCQNSEFDRNMEGASCFISPGVLXNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PLGPIPARCEDYEIEIREDDTT---
                                                                     EGT-RLSIQWEKPVSAFPIHCFDYEVKIHNTRNGYLQIEKLMTNAFISIIDDLSKYDVQV
                                                                                                     ESSCEIKLKWSIPLGPIPARCFDYEIEIREDDTTLVTATVENETYTLKTTNETROLCFVV
                                                                                                                                                                         -GQNIGCREP--YLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLPPVYLTFTR
                                                                                                                                                                                                                                                                                                                                                                                                                           89;
                                                                                                                                                                                                                                              -----YYNWQYLL-CSWKPGIGVLLDTNYNLFY----WYEGLDHALQCVDYIKAD
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28.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 292; DB 2,
No. 1.2e-15;
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F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-831/Product: prolactin receptor #status predicted <MAT>
F;36-219/Domain: cytokine receptor homology <CRS1>
F;239-425/Domain: cytokine receptor homology <CRS2>
F;439-462/Domain: transmembrane #status predicted <TMM>
F;549-462/Domain: transmembrane #status pre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          perleukin-5 receptor - mouse
perles: Mus musculus (house mouse)
paties: 11.Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Jun-2000
pate: 21.Nov-1993 #sequence_revision 10-Nov-1995 #text_change 20-Jun-2000
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Best Local
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VTPLHEGFAASVRTILK---SSHTTLASSWVSAEL-KAPPGSPGTSVTNLTCTTHTVVSS
                                                            GFDLNKGIEAKIHTLLPWQCTNGSEVQSSWAETTYWISPQGIPETKVQDMDCVYYN----
                                                                                                                                                                                                   PPQDFEIVDPGYLGYLYLQWQPPLSLDHFKECTVEYELKYRNIGSETWKTIITKNLHYKD
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                                                                                                                                   PPVNFTIKATG-LAQVLLHWDPNPDQEQ-RHVDLEYHVKINAPQEDEYDTRKTES---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LPPVYLTFTRESSCEIK----LKWS-IPLGPIPARCFDYEIEIR---EDDTTLVTATVEN 290
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                                                                                                                                                                                                                                                                              l Similarity
91; Conser
                                                                                                                                                                                                                                                                                                                                                                                                           cytokine receptor; transmembrane protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1-415 <TAK>
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                                                                                                                                                                                                                                                                                                       Score 247; DB 2;
Pred. No. 5.8e-12;
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Pred. No. 7.6e-13;
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                                                                                                                                                                                                                                                                           151;
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                                                                                                                                                                                                                                                                                                                                       Length 415
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97 LNKGIEAKIHTLLPWQCTNGSE-VQSSWAETTYWISPQGIPETKVQDMDCVYYNWQYLLC 155

-- PNGNEDTTADFFLTTMPTDSLSVSTLPLPEVQCFVFNVEYMNC

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A;Cross-references: GDB:134807; OMIM:308380
A;Map position: Xq13.1-Xq13.1
A;Introns: 39/1; 90/2; 152/1; 198/3; 253/1; 285/2;
A;Introns: are associated with an X-linked for C;Superfamily: interleukin-2 receptor gamma chain C;Keywords: cytokine receptor; duplication; immunoc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Homo sapiens (man)
C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000
C;Accession: A42565; A46591; T54332
                                                                                                                                                                                                                                                                                                                                                                                    Hum. Mol. Genet. 2, 1099-1104, 1993
A;Title: The interleukin-2 receptor gamma chain maps to A;Reference number: I54332; MUID:94004847; PMID:8401490
A;Accession: I54332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:L12183; NID:g307056; PIDN:AAA59145.1; PID:g307058 R;Puck, J.M.; Deschenes, S.M.; Porter, J.C.; Dutra, A.S.; Brown, C.J.; W Hum. Mol. Genet. 2, 1099-1104, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Noguchi, M.; Adelstein, S.; Cao, X.; Leonard, W.J. J. Biol. Chem. 268, 13601-13608, 1993
A;Title: Characterization of the human interleukin-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R; Takeshita, T.; Asao, F
Science 257, 379-382, 19
A; Title: Cloning of the
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                                                                                                                                                                                                                                                A; Gene: GDB:IL2RG; SCIDX1; IMD4
                                                                                                                                                                                                                                                                       C; Genetics:
                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-369 < RE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Reference number: A46591; MUID:93293887; A; Accession: A46591
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: MOLT beta lymphoid cells
A; Note: sequence extracted from NCBI backbone (NCBIP:109167)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:D11086; NID:g303611; PIDN:BAA01857.1; PID:g219890
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Title: Cloning of the gamma chain of the A; Reference number: A42565; MUID:92335883;
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                                                                                                                                                                                                                                                                                              A;Cross-references: GB:L19546; NID:g349631; PIDN:AAC37524.1;
                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
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A; Residues: 1-369 < RES>
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     Similarity
70; Conser
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                         10.5%;
Score 220; DB 2;
Pred. No. 6.9e-10;
8; Mismatches 121;
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PMID:8514792
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PMID:1631559
                                                                                             immunodeficiency; severe
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form of s
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  36;
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F:36-220/Domain: c
F:240-426/Domain:
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C;Species: ^-_ ''^^^ *comence_revision 13-Sep-1996 #text_change
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C:Superfamily: cytokine receptor homology
F:36-220/Domain: cytokine receptor homology <CRS1>
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A; Residues: 1-830 <CHE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPPPLADVTSNSHVYRYELRLKPEEKEEWETV---SVGVQTQYKVNR-LQAGVKYVVQVR 206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VTYIVQTDPPVNVTLELKKTVNRKPYLVLTWSPPPLADVRSGWLTLDYELRLKPEEA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LQNIVKPLPPVYLTFTRESSCEIK----LKWS-IPLGPIPA--RCFDYEIEIREDDTTLV 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LYSKEGEERVYECPDY-KTAGPN-SCYFDKKHTSFWTIYNITVKATNEIGSNVSDPLYVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CVLDIGEWSEWSSERHIHIPNGESPPEKPTIIKCRSPEKETFTCWWKPGSDGGHPTNYTL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TTYNITVMAMNEIGSNSS------DPQYVDVTSIVQPDAPVNLSLETKTSASTTYLLAKW 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QTFVVQLQDPRE--PRRQATQMLKLQNLVIPWAPENLTLHKLSESQLELNWN---NRFLN 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KDFYICVNGSSENKPIRSSYFTFQLQNIVKPLPPVYLTFTRESSCEIKLKWSIPLGPIPA 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SW-----KPGIGVLLDTNYNLFYWYEGLDH--ALQCVDYIKADGQNIGCRFPYLEASDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        l Similarity
93; Conserv
      receptor gamma
s musculus (hous
                                                                                                                                                                                                                                                                                                                                        -EEWETIFVGQQTHYKMFSLNPGKKYIVQIHCKPDHHGSWSEWSLEKYLQIPTDFR 436
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          (house
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                                     chain
      main precursor mouse)
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Gene 130, 303-304, 1993
A; Title: Cloning and sequencing of the cDNA encoding a markeference number: JN0775; MUID:93366191; PMID:8359699
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                                                                                                                                                                                                                                                                                                               A;Description: receptor for interleukin-2
A;Description: receptor for interleukin-1
A;Pathway: interleukin-2 stimulated growth and differentiation of T cell
C;Superfamily: interleukin-2 receptor gamma chain
C;Keywords: cytokine receptor; duplication; glycoprotein; transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references:
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;DiSanto, J.P.; Certain, S.; Wilson, A.; MacDonald, H.R.; Avner, Eur. J. Immunol. 24, 3014-3018, 1994
A;Title: The murine interleukin-2 receptor gamma chain gene: organ A;Reference number: I53398; MUID:95104285; PMID:7805729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Chiu, R.K.; Dougherty, G.J. submitted to the EMBL Data Library, October 1993 submitted to the EMBL Data Library, October 1993 A;Description: Regulation of CD44-mediated cellular adhesion
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C; Complex:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-350,'S',352-366,'S',368-369
A; Cross-references: EMBL: X75337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: S37582
A; Accession: S37582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-369 < KOB>
A; Cross-references: GB:D13821; NID:g436045; PIDN:BAA02974.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: DDBJ:D13565; NID:g303684; PIDN:BAA02760.1; R;Kobayashi, N.; Nakagawa, S.; Minami, Y.; Taniguchi, T.; Kono
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: nucleic acid sequence not shown A;Molecule type: mRNA A;Residues: 1-369 <KUM>
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Proc. Natl. Acad. Sci. U.S.A. 90, 8464-8468, 1993
A;Title: Characterization of cDNAs encoding the murine
                                                                                                                                                                                                                                          F;23-369/Product: interleukin-2 receptor gamma chain #s
F;256-284/Domain: transmembrane #status predicted <TMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                C; Function
                                                                                                                                                                                                                                                                                                                                                                                                                                                         eptors
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A; Residues: 1-369 < RES>
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A; Residues: 1-369 < RE2>
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A; Residues: 1-369 < CAO>
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C;Accession: 149280; A47514; JN0592; JN0775; S37582; I53398
                                                                                                                                                                                                            F;71,75,84,96,159,164,306/Binding site: carbohydrate (Asn) (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: IL-2Rgamma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                           Matches
                                                                                                                                                                                                                                                                                         22/Domain: signal sequence #status predicted <SIG>
                                                    136 PETKVQDMDCVYYNWQYLLCSW----KPGIGVLLDTNYNLFYWYEGLDHAL--QCVDYIK 189
53
                                                                                                                                    Local Similarity
PTLPLPEVQCFVFNIEYMNCTWNSSSEPQA---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39/1; 90/2; 152/1; 199/3; 254/1; 286/2; 308/3 The high affinity receptor is a heterotrimer
                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GB:S75852; NID:g861554; PIDN:AAB32904.1;
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                                                                                                                                 10.1%;
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                                                                                                        43;
                                                                                                                                                                                                                                                                receptor gamma chain #status predicted
                                                                                                                                 Score 212.5; DB 2
Pred. No. 2.7e-09;
                                                                                                        Mismatches
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o, H.; Nakamura, N
TNLTLHYRYKVSDNNTFQECSHYLF
                                                                                                                                                             DB 2;
                                                                                                           116;
                                                                                                                                                          Length
                                                                                                        Indels
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                                                                                                        23;
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interleukin-2 receptor gamma chain precursor - dog
C;Species: Canis lupus familiaris (dog)
C;Species: Canis lupus familiaris (dog)
C;Accession: A55718
C;Accession: A55718
R;Henthorn, P.S.; Somberg, R.L.; Fimiani, V.M.; Puck, J.M.; Patterson, D.F.; Fel
Genomics 23, 69-74, 1994
A;Title: IL-2Rgamma gene microdeletion demonstrates that canine X-linked severe A;Accession: A55718; MUID:95130114; PMID:7829104
A;Accession: A55718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-373 <HEN>
A; Cross-references: GB:U04361; NID:g517411;
C; Superfamily: interleukin-2 receptor gamma
C; Keywords: cytokine receptor; duplication
                                                                  interleukin-3 receptor beta chain precursor - mouse C;Species: Mus musculus (house mouse) C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #C;Accession: A40091; A43022 R;Itoh, N.; Yonehara, S.; Schreurs, J.; Gorman, D.M. Science 247, 324-327, 1990
                                                                                                                                                                                RESULT 10
A40091
A;Reference number: A40091;
A;Accession: A40091
A;Status: nucleic acid seque
                                  A; Title: Cloning of an interleukin-3 receptor gene: a m A; Reference number: A40091; MUID:90117145; PMID:2404337
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GVLLDTNYNLFYWYEGL--DHALQCVDYIKADGQNIGCRFPYLEASDYKDFYICVNGSSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NGNEDITPDFFLTATPSET---LSVSSLPLPEVQ---CFVFNVEYMNCTWNSSSEPRP--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NGSE-----VQSSWAETTYWISPQGIPETKVQDMDCVYYNWQYLLCSW-----KPGI 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SKEITSGCQIQKEDIQLYQTFVVQL--QDPQKPQRRAVQKLNLQNLVIPRAPENLTLSNL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VRSKVNIYCSDDGIWSEWSDKQCWEG----EDLSKKTLLRFWLPFGF--ILILVIFVTGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SESQLELRWK - - SRHIKERCLQYLVQYRSNRDRSWTELIVNHEPRFSLPSVDELKRYTFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADGQNIGCREPYLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLPPVYLTFTRE
                                                                                                                                                                                                                                                        KENPLFASEAVLIPLGSMGLIISLI
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                                                                                                                                                                                                                                                                                                                               WDRSWTEQSVDHRNSFSLPSVDGQKFYTFRVRSRYNPLCGSAQRWSEWSHPIHW~GSNTS
                                                                                                                                                                                                                                                                                                                                                                                                                                         NKPIRSSYFTFQLQNIVKPLPPVYLTFTRESSCEIKLKWSIPLGPIPARCFDYEIEIRED
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                                                                                                                                                                                                                                                                                                                                                                                                       --PRRQSTQKLKLQNLVIPWAPENLTLHNLSESQLELSWS---NRHLDHCLEHVVQYRSD
                                                                                                                                                                                                                                                                                                                                                                 -DTTLVTATVEN-ETYTLKTTNETRQLCFVVRSKVNIYCSDDGIWSEWSDKQCWEGEDLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TNLTLHYWYKNSNDDKVQECGHYLFSREVTAGCWLQKEEIHLYETFVVQLRDPRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
sequence
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26.0%;
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 not shown
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                                                                                                                                                                                                                                                                                            358
                                                                                                                           30-Jun-1993 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     chain
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                                                                                       D.M.; Maruyama,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length
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                                                                                     K.; Ishii,
                                                                                                                           22-Jun-1999
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                                                     receptor gene
                                                                                       Α.;
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                                                                                         Yahara,
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                                                                                                                                                                                                                                                                                                             C; Accession: A39255
                                                                                                                                                                                                                                                                                                                           C;Species: Homo sapiens (man)
C;Date: 30-Jun-1993 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                               cytokine receptor common beta chain precursor
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-815, 'Q', 817-878 <GOR>
A; Cross references: GB: M29855; NID: 9198342; PIDN: AAA39295.1; PID: 9309406
A; Cross references: GB: M29855; NID: 9198342; PIDN: AAA39295.1; PID: 9309406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: interleukin-3 receptor beta chain; cytokine r C;Keywords: cytokine receptor; duplication; transmembrane pr F;1-22/Domain: signal sequence #status predicted <SIG> F;23-878/Product: interleukin-3 receptor beta chain #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: A; Accession: A43022
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to GenBank,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F;463-878/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              F;441-462/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F; 254-433/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                F;23-440/Domain: extracellular #status predicted <EXT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local Similarity
415
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                                                                                                                                     254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D.M.
VRVKPISDY - - - DGIWSEWSNEYTWT-TDWVMPTL- - - WI - - - - VLILVFLIFTLLL
                                                                                       YSLHWETQKIP----KYIDHTFQVQYKKKSESWKDSKTENLGRVNSMDLPQLEPDTSYCAR 414
                                                                                                                                  IKLKWSIPLGPIPARCED--YEIEIREDDTTLVTATVEN----ETYTLKTTNETRQLCFV 307
                                                                                                                                                                                                                                                                             QPQNLQCFFDGIQSLHCSWEVWTQTTGSVSFGLFYRPSPAAPEEKCSPVVKEPQASVYTR
                                                                                                                                                                                                                                                                                                                        KVQDMDCVYYNWQYLLCSWKPGIGVLLDTNYNLFYWYEGLDHALQCVDYIKADGQNI----
                                                                                                                                                                                                                                                                                                                                                                                                                  YKDGFDLNKGIEAKIHTLLP------WQCTNGSEVQ---SSWAETTYWISPQGIPET 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPKDIHISPSG--DHFLLEWSVSLGDSQVSWLSSKDIEFEVAYKRL-QDSWED--ASSLH 193
                                         VRSK-VNIYCSDDGIWSEWSDKQCWEGEDLSKKTLLRFWLPFGFILILVIFVTGLLL
                                                                                                                                                                                   YRCSLPVPEPSAHSQYTVSVKHLEQGKFI-MSYYHIQME----PPILNQTKNRDS---
                                                                                                                                                                                                                                                                                                                                                                      -TSNFQVN--LEPKL--FLPNSIYAARVRTRLSAGSSLSGRPSRWSPEVHWDSQPG-DKA
                                                                                                                                                                                                                            -GCRFPYLEASDYKDFYICVNGSSENKPIRSSYFTFQLQNIVKPLPPVY-LTFTRESSCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86;
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transmembrane #status predicted <TMM>
intracellular #status predicted <INT>
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24.1%;
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Pred. No. 2e-07
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A:Cross-references: GDB:126838; OMIM:138981
A:Map position: 22q13.1-22q13.1
C:Superfamily: interleukin-3 receptor beta chain; cytokine receptor homology C:Keywords: alternative splicing; cytokine receptor; duplication; transmembr: E:1-16/Domain: signal sequence #status predicted <SIG>
F:17-897/Product: cytokine receptor common beta chain #status predicted <MAT: R;Hayashida, K.; Kitamura, T.; Gorman, D.M.; Arai, K.; Yokota, T.; Miyajima, Proc. Natl. Acad. Sci. U.S.A. 87, 9655-9659, 1990
A;Title: Molecular cloning of a second subunit of the receptor for human grand, Reference number: A39255; MUID:91088571; PMID:1702217 A; Gene: GDB:CSF2RB C; Genetics: A;Cross-references: GB:M38275 C;Comment: The human high-affinity A; Molecule type: mRNA A; Residues: 1-897 <HAY> A; Accession: A39255 IL-3, IL-5, and GM-CSF receptors transmembrane have granulocyteligand-speci

AMAT:

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30-Jun-1993 #text\_change 02-Sep-1997

human

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F;17-443/Domain: (F;35-232/Domain: (F;250-431/Domain: F;444-460/Domain: F;461-897/Domain:
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A;Title: Cloning of rat interleukin-3 receptor beta-subunit A;Reference number: I56563; MUID:95370942; PMID:7643220
A:Accession: I56563
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                                                                                                                                                                                                                                                                                                                                Superfamily: interleukin-3 receptor beta chain; cytokine 
Keywords: cytokine receptor 
39-235/Domain: cytokine receptor homology <CRS1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;Species: Rattus sp. (rat)
;Date: 26-Jul-1996 #sequence_revision
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;444-460/Domain:
                                                                                                                                                                                                                                                                                                            253-433/Domain: cytokine receptor homology <CRS2>
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                                                                                                                                                                                                                                                             Query Match
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Best Local
                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cross-references: GB:S79263; NID:g1086954; PIDN:AAB35068.1; PID:g1086955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         atus: preliminary; translated
lecule type: mRNA
Residues: 1-896 <RES>
                   152 LLKWSVPLGDAQVSLLSQKDIQFEVAYKQL-QDSWED--ASSLH-----TCNLWVTLEPK
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                                                                  50 YLQWQPPL---SLDHFKECTVEYELKYRNIGSETWKTIITKNLHYKDGFDLNKGIEAKIH 106
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                                                                                                                                                                                                                                         Local
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                                                                                                                                                   CLAIGCL--YT-FLISTTFGCTSSSDTEIKVN----------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VASSVSFGLFYKPSPDAGEEECSPVLR---EGLGSLHTRHHCQIPVPDPATHGQYIVSVQ 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      KIHT-LLPWQCTNGSEVQSSWAETTYWISPQGIPETKVQDMDCVYYNWQYLLCSWKPGIG 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GSPQSHWLSPGDLEFEVVYKRL-QDSWEDAAILLSNTS----QATLGPEHLMPSSTYVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VIPCQSEVVTDVDYFSFQPDRPLGTRLTVTLTQHVQPPEPRDLQISTDQDHFLLTWSVAL
                                                                                                                 CVPRRCVLPYTQFSVSKEDYYSLQPDRDLSIHLVVPLAQHVQPPPPKDISISPSG--DHF 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WSEARSWDTESV-----LPMWVLALIVIFLTTAVL 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WSDKQCWEGEDLSKKTLLRFWLPFGFILILVIFVTGLLL 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YRKD----TATWKDSKTETLQNAHSMALPALEPSTRYWARVRVRTSRTGY---NGIWSE 427
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VLLDTNYNLFYWYEGLDHALQCVDYIKADGQNIG-----CRFPYLEASDYKDFYICVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RVRTRLAPGSRLSGR--PSKWSPEVCWDSQPG-DEAQPQNLECFFDGAAVLSCSWEVRKE 267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----KECTVEYELKYRNIGSETWK--TIITKNLHYKDGFDLNKGIE------A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSSENKPIRSSYFTFQLQNIVKPLPPVYLTFTRESSCEIKLKWSIPLGPIPARCFDYEIE
                                                                                                                                                                                                                   87; Conser
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cytokine receptor homology <CRS1>
cytokine receptor homology <CRS2>
transmembrane #status predicted <TMM>
                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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22.6%; Pred. No. 2.9e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           58; Mismatches 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from
                                                                                                                                                                                                                                       Score 178; DB 2;
Pred. No. 4.6e-06;
                                                                                                                                                                                                                 Mismatches 167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rat
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                                                                                                                                                                  -PPQDFEIVDPGYLGYL
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A; Residues: 1-896 <GOR>
A; Residues: 1-896 <GOR>
A; Cross-references: GB:M34397; NID:g191821; PIDN:AAA37204.1; PID:g309101
C; Comment: Mouse high-affinity IL-5, GM-CSF, and one class of high-affinity IL-3
C; Superfamily: interleukin-3 receptor beta chain; cytokine receptor homology
C; Keywords: cytokine receptor; duplication; transmembrane protein
F; 1-22/Domain: signal sequence #status predicted <SIG>
F; 23-896/Product: cytokine receptor common beta chain #status predicted <MAT>
F; 23-441/Domain: extracellular #status predicted <EXT>
F; 39-235/Domain: cytokine receptor homology <CRS1>
F; 39-235/Domain: cytokine receptor homology <CRS1>
F; 39-235/Domain: cytokine receptor homology <CRS1>
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R;Gorman, D.M.; Itoh, N.; Kitamura, T.; Schreurs, J.; Yonehara, S.; Yahara, I.; Ar Proc. Natl. Acad. Sci. U.S.A. 87, 5459-5463, 1990
A;Title: Cloning and expression of a gene encoding an interleukin 3 receptor-like A;Reference number: A35782; MUID:90319131; PMID:1695379
A;Accession: A35782
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytokine receptor common beta chain precursor - mouse
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999
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VQYKKKSDSWEDSKTENLDRAHSMDLSQLEPDTSYCARVRVKPISNYDGIWSKWSEEYTW
                                            IEIREDDTTLVTATVEN--ETYTLKTTNETRQLCFVVRSKVNIYCSDDGIWSEWSDKQCW 331
                                                                                           V-----KHLEQGKFIMSYNHIQMEPPTLNLTKNRDS---YSLHWETQKMAYSFIEHTFQ
                                                                                                                                       VNGSSENKPIRSSYFTFQLQNIVKPLPPVYLTFTRESSCEIKLKWSIPLGPIPARCFDYE
                                                                                                                                                                                                                                    PGIGVLLDTNYNLFYWYEGLDHALQCVDYIK-ADGQNI----GCRFPYLEASDYKDFYIC
                                                                                                                                                                                                                                                                                   IYAPRVRTRLYPGSSLSGR--PSRWSPEAHWDSQPG-DKAQPQNLQCFFDGIQSLHCSWE
                                                                                                                                                                                                                                                                                                                                IEA-KIHT-LLPWQCTNGSEVQSSWAETTYWISPQGIPETKVQDMDCVYYNWQYLLCSWK 158
                                                                                                                                                                                                                                                                                                                                                                              FLLEWSVSLGDAQVSWLSSKDIEFEVAYKRL-QDSWEDAYSLHTSKFQVNFEPKLFLPNS
                                                                                                                                                                                                                                                                                                                                                                                                                           LYLOWOPPL---SLDHFKECTVEYELKYRNIGSETWKTIITKN-----LHYKDGFDLNKG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CVPRRCVIPY---TRFSITNEDYYSFRPDSDLGIQLMVPLAQNVQPPLPKNVSISSSEDR 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLAIGCLYTFLISTTFGCTS-----SSDTEIK-----VNPPQDFEIVDPGYLGY
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                                                                                                                                                                                        VWTQTTGSVSFGLFYRPSPVAPEEKCSPVVKEPPGASVYTRYHCSLPVPEPSAHSQYTVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81;
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Similarity 20.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 173.5; DB 1;
Pred. No. 1e-05;
9; Mismatches 185;
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438 K-TDWVMPTL---WI----VLILVFLILTLLL

363 461

EGEDLSKKTLLRFWLPFGFILILVIFVTGLLL

10;

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prolactin receptor Nb2 precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C:Species: Rattus norvegicus (Norway rat)
C:Accession: A41070; 155417; P.A.
C:Accession: A41070; 155417
R:Ali, S: Pellegrini, I: Kelly, P.A.
J. Biol. Chem. 266, 20110-20117, 1991
A:Title: A prolactin-dependent immune cell line (Nb2) expresses a mutant form of A:Reference number: A41070; MUID:92041834; PMID:1718958
A:Accession: A41070
A:Molecule type: mRNA
A:Residues: 1-412 <ALL>
A:Cross-references: GB:M74152; NID:9206389; PIDN:AAA41946.1; PID:9206390
A:O'Neal, K.D.; Yu-Lee, L.Y.
J. Biol. Chem. 269, 26076-26082, 1994
A:Title: Differential signal transduction of the short, Nb2, and long prolactin A:Reference number: 155417; MUID:95014432; PMID:7929319
A:Accession: 155417
A:Status: translated from GB/EMBL/DDBJ
A:Rocsidues: 1-412 <RES>
A:Cross-references: EMBL:U07567; NID:9641963; PIDN:AAA61784.1; PID:9641964
A:Experimental source: Nb2-11C cell line
C:Superfamily: Cytokine receptor homology
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A;Title: Cloning and expression of the rat prolactin receptor, a member of the garacteric number: A29884; MUID:88165059; PMID:2832068
A;Accession: A29884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  prolactin receptor precursor - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 28-Jul-2000
C;Accession: A29884
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C:Keywords: transmembrane protein
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Best Local :
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esidues: 1-310 <BOU>
Cross-references: GB:M19304; NID:g206364; PIDN:AAA41937.1; PID:g206365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           246 F----TRESSCEIKLKWSIP-LGPIPARCFDYEIEIREDDTTLVTATVENETYTLKTTNE 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     301 TRQL-----CFVVRSKVNIYCSDDGIWSEWSDKQCWE 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      76 SGPN-SCFFSKQYTSIWKIYIITVNATNQMGSSSSDPL----YVDVTYIVEPEPPRNLT 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QTQFKVFDLYPGQKYLVQTRCK---PDHGYWSRWSQESSVE 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LEVKQLKDKKTYLWVKWSPPTITDVKTGWFTMEYEIR-----LKPEEAEEWEIHFTGH 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DGQNIGCRFPYLEASDYKDFYICVN-----GSSENKPIRSSYFTFQLQNIVKPLPPVYLT 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 7.8%; Score 165; DB Similarity 28.5%; Pred. No. 1.3e 63; Conservative 24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 165; DB 2; 2.
Pred. No. 1.3e-05;
Prematches 94;
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                                           301
                                                                                 130 LEVKQLKDKKTYLWVKWSPPTITDVKTGWFTMEYEIR-----LKPEEAEEWEIHFTGH 182
                                                                                                                        246 F----TRESSCEIKLKWSIP-LGPIPARCFDYEIEIREDDTTLVTATVENETYTLKTTNE 300
                                                                                                                                                                                                               191 DGQNIGCRFPYLEASDYKDFYICVN-----GSSENKPIRSSYFTFQLQNIVKPLPPVYLT 245
183 QTQFKVFDLYPGQKYLVQTRCK---PDHGYWSRWSQESSVE 220
                                                                                                                                                                        76 SGPN-SCFFSKQYTSIWKIYIITVNATNQMGSSSSDPL----YVDVTYIVEPEPPRNLT 129
                                                                                                                                                                                                                                                              21 SPPGKPEIH----KCRSPDKETFTCWWNPGTDGGLPTNYSLTYSKEGEKTTYECPDY-KT 75
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                                  -CFVVRSKVNIYCSDDGIWSEWSDKQCWE 332
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